71 71

17.5 17.5

3**74** 353  $\mu$ 

R82490 R81587

Cry j I Japanese C Cedar pollen aller

GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 29, 1999, 13:01:00; Search time 40.75 Seconds (without alignments) 46.500 Million cell updates/sec

Title: Perfect score: Sequence: US-09-142-524-1 406 1 MKVTVAFNQFGPNRRVFIKR.....IASRRVDGIIAAYQNPASWK 80

Scoring table: BLOSUM62

Searched: 188963 seqs, 23686106 residues

Database : A\_Geneseq\_36:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

31 33 34 35 35 35 37 37 38 41 41 41 42 43	222222222222 20122222222222222222222222	10 11 13 13 15 16 17	4GW4NDF8	ZC
74 74 74 73 73 73 71 71 71 71 71 71	744	1 t t 4	27.	iğ
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1 W04345 W42122 1 W42122 1 R45588 1 R45577 1 R97907 1 R97907 1 R31937 1 R4586 1 R4587 1 R4587	<<< m < m < m < m < m < x < x < x < x <	<b>៩៩៩៩៦៦៦៦៦</b> ៦៦	********	ID
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Synthetic.

W09732600-A1.

12-SEP-1997.

10-MAR-1997.

10-MAR-1997.

10-MAR-1996: JF-080702.

(MEIP) MEIJI MIKE PROD CO LTD.

Dalriki K, Iwama A, Kino K, Kume A, Sone T;

Peptide immuno:therapeutic agent to treat allergic diseases contains multi-epitope peptide containing T cell epitope regions

from different allergens

Claim 6; Page 31; 58pp; Japanese.

RES W2 ID AC AC DT DE KW KW	Qy Qy Qy Qy	RESULT W27369 ACC ACC ACC ACC ACC ACC ACC ACC ACC AC	
RESULT 2  W27370 ID W27370 standard; peptide; 105 AA.  AC W27370; DT 24-MAR-1998 (first entry) DE Multi-epitope peptide used as immunotherapeutic agent #2.  KW Multi-epitope peptide; immunotherapeutic agent; allergic disease;  KW T-cell epitope region; allergen; lymphocyte; immunoglobulin E.  OS Synthetic.	Best Local Similarity 100.0%; pred. No. 4.26-40; Indels 0; Gaps 0; Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  1 MKVTVAFNQFGPNRRVFIKRVSNVIIHGRRIDIFASKNFHLQKNTIGTGRRISLKLTSGK 60	1 27369 standard; peptide: 80 AP 27369; 4-MAR-1998 (first entry) 4-MAR-1998 (first entry) 4-MAR-1998 (first entry) 4-MAR-1998 (first entry) 4-MAR-1998 (peptide used as i ulti-epitope peptide: imunoti -cell epitope region; allerger ynthetic. 109732600-A1. AP 2-SEP-1997; J00740. 0-MAR-1997; J00740. 0-MAR-19	ALIGNMENTS

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Best Local
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                                                                                                                                                                                                                                                                             The present sequence represents a multi-epitope peptide which is used as a new immunotherapeutic agent. It comprises I cell epitope regions from 2 or more different allergens (preferably linked via arginine or lysine dimers), where the T cell epitope regions: have a positivity index allergen; have at least 70% reactivity with lymphocytes from patients responding to the allergen; and are not reactive with immunoglobulin E (19E) antibodies from patients responsive to the allergen. The agent can be used to prevent and treat a wide variety of allergic diseases, e.g. by common 124 has side effects, e.g. those mediated by 19E, are reduced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from different allergens
Claim 6; Page 32; 58pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide immuno:therapeutic agent to treat allergic diseases contains multi-epitope peptide containing T cell epitope regions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MEIP ) MEIJI MILK PROD CO LTD.
Dairiki K, Iwama A, Kino K, Kume A, Sone T;
WPI; 97-470495/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-SEP-1997.
10-MAR-1997; J00740.
10-MAR-1996; JP-080702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Multi-epitope peptide used as immunotherapeutic agent #3.
Multi-epitope peptide; immunotherapeutic agent; allergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W27371 standard; peptide; 134 AA. W27371; 24-MAR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents a multi-epitope peptide which is used as a new immunotherapeutic agent. It comprises T cell epitope regions from 2 or more different allergens (preferably linked via arginine or lysine dimers), where the T cell epitope regions: have a positivity index greater than 100 as measured in a patient group responding to the allergen; and are not reactive with immunoglobulin E responding to the allergen; and are not reactive with immunoglobulin E (IGE) antibodies from patients responsive to the allergen. The agent can desensitisation. Side effects, e.g. those mediated by IGE, are reduced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
W09732600-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T-cell
                                    61 FAKLTGETLMGRRPLWIIFSGNMNIKLKMPMYIAGYKTEDGRRAEVSYVHVNGAKFIRRV 120
                                                                                        52 ----
                                                                                                                             1 MKVTVAFNQFGPNRRVFIKRVSNVIHGRRIDIFASKNFHLQKNTIGTGRR------ 52
                                                                                                                         H
                                                                                                                                                                                                              Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 FAKLTGFTLMGRRLKMPMYIAGYKTFDGRRVDGIIAAYQNPASWK 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54 -LKLTSGKIA-------SRRVDGIIAAYQNPASWK 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MKVTVAFNQFGPNRRVFIKRVSNVIIHGRRIDIFASKNFHLQKNTIGTGRRWKNNRIWLQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MKVTVAFNQFGPNRRVFIKRVSNVIIHGRRIDIFASKNFHLQKNTIGTGRRIS----- 54
                                                                                                         MKVTVAFNQEGPNRRVEIKRVSNVIIHGRRIDIFASKNFHLQKNTIGTGRRWKNNRIWLQ 60
                DGIIAAYQNPASWK 80
Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     region; allergen; lymphocyte; immunoglobulin
                                                                                                                                                                                                       78.8%;
53.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80.7%;
                                                                             ----ISLKL-----
                                                                                                                                                                                                   Score 320; DB 1
Pred. No. 4e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 327.5; DB 1
Pred. No. 2.8e-37;
                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                  DB 1; Length 134;
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                                                                           ------TSGKIASRRV 66
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                                                                                                                                                                                  Indels
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                                                                                                                                                                               54;
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        Matches
                    Best Local
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                                                                           Claim 10; Page 5; 21pp; Japanese.
W80339-58 represent epitopes for T cells, derived from the sugproteins Cryj1 (W80339-44, W80350-53 and W80356-58) and Cryj2 and W80354-55). The peptides are useful for the treatment of sugi-pollinosis, an allergic reaction of the body to pollen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sugi-pollinosis
Claim 10; Page 5; 21pp; Japanese.
Claim 10; Page 5; 21pp; Japanese.
W80339-58 represent epitopes for T cells, derived from the sugi allergen proteins Cryj1 (W80339-44, W80350-53 and W80356-58) and Cryj2 (W80345-49 and W80354-55). The peptides are useful for the treatment of sugi-pollinosis, an allergic reaction of the body to pollen.
Sequence 47 AA;
                                                                                                                                                             sugi-pollinosis
                                                                                                                                                                                                                                                                       Synthetic.
J10259198-A.
                                                                                                                                                                                                                                                                                                   sugi-pollinosis; allergic
                                                                                                                                                                                    (HAYB) HAYASHIBARA SEIBUTSU KAGAKU
(SANY) SANKYO CO LTD.
WPI: 98-577037/49.
                                                                                                                                                                                                                               22-DEC-1997; 353448.
24-DEC-1996; JP-343441.
                                                                                                                                                                                                                                                                                                                                                                   W80358 standard; peptide; 81 AA.
                                                                                                                                                                                                                                                                                                                                              11-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A linked T cell epitope peptide - used for the treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HAYB) HAYASHIBARA SEIBUTSU KAGAKU (SANY) SANKYO CO LTD.
WPI; 98-577037/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sugi-pollinosis; allergic reaction; pollen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-DEC-1997;
24-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W80353 standard; peptide; 47 AA W80353;
                                                                                                                                                                 linked T cell epitope peptide - used for the treatment of
                                                                                                                                                                                                                                                                                            ugi allergen protein Cryj1 derived epitope for T cells cell epitope; sugi allergen proteins Cryj1; Cryj2; trugi-pollinosis; allergic reaction; pollen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J10259198-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 MKVTVAFNQFG------FASKNFHLQKNT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ll-JAN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                               36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 IASRRVDGIIAAYQNPASW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 DGIIAAYQNPASWK 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cell epitope; sugi allergen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MKVTVAFNQFGPNRRVFIKRVSNVIIHGRRIDIFASKNFHLQKNTIGTGRRISLKLTSGK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                          ------GIIAAYQNPASW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           allergen protein
                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35.
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     Conservative
                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JP-343441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              353448.
                33.3%;
46.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cryj1 derived epitope for T cells.
allergen proteins Cryj1; Cryj2; treatment;
             Score 135; DB 1, Pred. No. 3e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 144; DB 1;
Pred. No. 8.9e-13;
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                          DB 1;
                                                                                                            derived from the sugi allergen W80356-58) and Cryj2 (W80345-49
  8
                            Length 81;
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 Indels
30;
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δÃ

1 MKVTVAFNQFGPNRRVFIKRVSNVIIHGRRIDIFASKNFHLQKNTIGTGRRISLKLTSGK 60

B

В Š

WESSEZ ID PROSESS SERVICE SERV

W80351  W80351  W80351;  W80351;  T1-JAN-1999 (first entry)  T cell epitope; sugi allergen proteins Cryj1; Cryj2; treatment;  W T cell epitope; sugi allergen proteins Cryj1; Cryj2; treatment;  W sugi-pollinosis; allergic reaction; pollen.  S Synthetic.  J10259198-A.  D 29-SEP-1998.  Y 22-DEC-1997; 353448.  T 22-DEC-1997; 353441.  A (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.  A (SANY ) SANKYO CO LTD.  A (SANY ) SANKYO CO LTD.  A (SANY ) SANKYO CO LTD.  B WPI; 98-577037/49.  Claim 10; Page 5; 21pp; Japanese.  Claim 10; Page 5; 21pp; Japanese.  W80339-8 represent epitopes for T cells, derived from the sugi allergen und w80354-59) and Cryj2 (W80345-49)  proteins Cryj1 (W80339-44, W80350-53 and w80356-58) and Cryj2 (W80345-49)  proteins Cryj1 (W80339-44, W80350-53 and w80356-58) and Cryj2 (W80345-49)  S Sequence 47 AA;	Query Match 30.9%; Score 125.5; DB 1; Length 47; Best Local Similarity 50.8%; Pred. No. 2.9e-10; Matches 32; Conservative 0; Mismatches 0; Indels 31; Gaps 2; Matches 32; Conservative 0; Mismatches 0;	M80352 standard; peptide; 47 AA.  W80352; 11-JAN-1999 (first entry) Sugi allergen protein Cryjl derived epitope for T cells. Sugi-ptope; sugi allergen proteins Cryjl; Cryj2; treatment; T cell epitope; sugi allergen proteins Cryjl; Cryj2; treatment; Synthetic. Synthetic. Synthetic. 29-SEP-1998. 29-SEP-1998; 353448. 22-DEC-1996; JP-343441. 24-DEC-1996; JP-343441. 25-SEP-1998 29-SEP-1998 39-58-77037/49. A linked T cell epitope peptide - used for the treatment of sugi-pollinosis Claim 10; Page 5; 21pp; Japanese. Claim 10; Page	
W80356 standard; peptide; 47 AA.  ID W80356; AC W80356; DT 11-JAN-1999 (first entry) Exception: Cryj1; Cryj2; treatment; Exception: Cryj1 (washister entry) Exception: Color of the treatment of proteins (Cryj1) DR WPI; 98-577037/49. DR WPI; 98-577037/49. DR WPI; 98-577037/49. DR WPI; 98-577037/49. DR WPI; 98-57037/49. Exception: Color of the treatment of sugi-pollinosis. Exception: Japanese. Exception: Color of the treatment of color of the sugi-pollinosis. Exception: Cryj1 (w80339-44, w80350-53 and w80356-58) and Cryj2 (w80345-49) Exception: Cryj1 (w80339-44, w80350-53 and w80356-58) and Cryj2 (w80345-49) Exception: Cryj1 (w80339-44, w80350-53 and w80356-58) and Cryj2 (w80345-49) Exception: Cryj1 (w80339-44, w80350-53 and w80356-58) and Cryj2 (w80345-49) Exception: Cryj1 (w80339-44, w80350-53 and w80356-58) and Cryj2 (w80345-49) Exception: Cryj1 (w80339-44, w80350-53 and w80356-58) and Cryj2 (w80345-49) Exception: Cryj1 (w80339-44, w80350-53 and w80356-58) and Cryj2 (w80345-49) Exception: Cryj1 (w80339-44, w80350-53 and w80356-58) and Cryj2 (w80345-49) Exception: Cryj1 (w80339-44, w80350-53 and w80356-58) and Cryj2 (w80345-49) Exception: Cryj1 (w80450-49) Ex	Query Match Query Match Query Match Query Match Best Local Similarity 40.5%; Pred. No. 1.6e-09; Best Local Similarity 40.5%; Pred. No. 1.6e-09; Matches 32; Conservative 2; Mismatches 1; Indels 44; Gaps 2.    MATCHES 32; Conservative 2; Mismatches 1; Indels 44; Gaps 2.   MATCHES 32; Conservative 2; Mismatches 1; Indels 44; Gaps 2.   MATCHES 32; Conservative 2; Mismatches 1; Indels 44; Gaps 2.   MATCHES 32; Conservative 2; Mismatches 1; Indels 44; Gaps 2.   MATCHES 32; Conservative 2; Mismatches 1; Indels 44; Gaps 2.   MATCHES 32; Conservative 2; Mismatches 1; Indels 44; Gaps 2.   Matches 32; Matches 1; Indels 44; Gaps 2.   Matches 32; Matches 1; Indels 44; Gaps 2.   Matches 32; Matches 1; Indels 44; Gaps 2.   Match	RESULT 8 W80357 W80357 standard; peptide; 47 AA.  ID W80357; AC W80357; AC W80357; BT 11-JAN-1999 (first entry) DT 11-JAN-1999 (first entry) DT 21-JAN-1999 (first entry) DT cell epitope; sugi allergen proteins Cryjl; Cryj2; treatment; Sugi allergen protein cryjl derived epitope for T cells.  Sugi allergen protein cryjl derived epitope for T cells.  Sugi pollinosis; allergic reaction; pollen.  Synthetic.	Query Match Query Match Best Local Similarity 58.7%; Pred. No. 1e-09; Matches 27; Conservative 4; Mismatches 4; Indels 11; Gaps 2; Matches 27; Conservative 4; Mismatches 4; Mismatch

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Query Match Best Local S Matches

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W80351
ID OSS
W80351
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Sugi allergen protein Cryjl derived epitope for T cells.
T cell epitope; sugi allergen proteins Cryjl; Cryj2; treatment;
Sugi-pollinosis; allergic reaction; pollen.
Synthetic.
J10259198-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W80351 standard; peptide; 47 AA.
                                                                                                                                                         29-SEF-1998.
29-SEF-1997; 353448.
24-DEC-1997; 353441.
24-DEC-1996; JF-343441.
(HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
(SANY ) SANYO CO LTD.
WPI; 98-577037/49
A linked T cell epitope peptide - used for the treatment of
Sugimpolinosis

Claim 10) Page 5; 21pp; Japanese.

Claim 10; Page 5; 21pp; Japanese.

W80339-88 represent epitopes for T cells, derived from the sugi aller;

W80339-84, W80350-53 and W80356-58) and Cryj2 (W80345:

proteins Cryj1 (W80339-44, W80350-53 and W80356-58) and Cryj2 (W80345:

proteins Cryj1 (W80339-44).

Proteins Cryj1 (W80339-44).

R80334-55). The peptides are useful for the treatment of sugi-pollinosis, an allergic reaction of the body to pollen.

Sequence 47 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 MKVTVAFNQFG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42 IAS 44
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Matches Query Match

10

0

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Query Match
---- Local Similarity
---- Conser-
                                                                                                                                                                                         26 JAN-1995.
15-JUL-1994; J01164.
16-JUL-1993; JP-177008.
01-SEP-1993; JP-217725.
07-APR-1994; JP-069336.
          with IgE antibody
Example 3; Pages 27-28; 46pp; Japanese.
Q84045 encodes R69792 Japonicum allergen, from which the antiallergic
peptides R69845-R69809 were derived. The peptides ability to inhibit
the cross-linking of an allergen, to an IgE antibody can be used in
the prevention and treatment of allergic diseases.
                                                                                                         (MEIP) MEIJI MILK PROD CO LTD.

Kino K, Kohno Y, Komiyama N, Sone T;

WPI; 95-067159/09.

N-PSDB; Q84045, Q84046.

Peptide antiallergic agent - inhibits cross-linking of allergen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pollinosis
Claim 2; Fig 4; 89pp; English.
The sequence is of a Japanese cedar pollen allergen Cry j
II. The protein and its fragments can be used for diagnosis and treatment of Japanese cedar pollinosis and to identify similar sequences in other plants.
Sequence 514 AA;
Sequence 514 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9411512-A.
26-MAY-1994.
12-NOV-1993; U11000.
12-NOV-1992; US-975179.
                                                                                                                                                                                                                                                                                 Japonicum allergen: """", Japonicum allergen; induced histamine release; antiallergic peptide; IgE cross-linking inhibition.
Japonicum sp.
                                                                                                                                                                                                                                                                                                                                            R69792;
27-SEP-1995
                                                                                                                                                                                                                                                                                                                                                               R69792 standard; Protein; 514
                                                                                                                                                                                                                                                                                                                                                                                                                                    236 IDIFASKNFHLQKNTIGTG 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Allergenic Cry j II protein and fragments from Japanese cedar pollen - used to diagnose, treat and prevent Japanese cedar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; Q66048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (IMMU-) IMMULOGIC PHARM CORP. Brauer A, Kuo M, Pollock J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cryptomeria japonica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Japanese cedar pollen allergen Cedar pollinosis; diagnostic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     31 IDIFASKNFHLQKNTIGTG 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R53690 standard; Protein; 514 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34 FASKNFHLQKNTIGTGRRISLKLTSGKIASRRVDGIIAAYQNPASWK 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 FASKNFHLQKNT-----
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                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24.4%; Score 99;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------GIIAAYQNPASWK 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 114; DB 1;
Pred. No. 1.1e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yeung S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
5. 2.5e-05;
0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 514;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
                                                    03-NOV-1994; 308117.
05-NOV-1993; JP-299151.
20-DEC-1993; JP-344596.
27-DEC-1993; JP-346614.
(HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
KUTIMOTO M, Namba M, TOTIGOE K;
WPI; 95-195588/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
New Japanese cedar pollen allergen polypeptide - and DNA coding useful for treatment and diagnosis of cedar pollen allergy Claim 5; Page 26-28; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                   Cryptomeria japonica.
EP-655500-A.
                                                                                                                                                                                                         Japanese cedar pollen allergen,
Japanese cedar; pollen; allergen; allergy; therapy; diagnostic;
                                                                                                                                                                                                                                                    01-NOV-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              with IgE antibody
Disclosure; Pages 26-27; 46pp; Japanese.
Q84044 encodes R69791 Japonicum allergen residues 55-514, from
which the antiallergic peptides R69845-R69809 were derived.
The peptides ability to inhibit the cross-linking of an allergen,
The period antibute of the cross-linking of an allergen,
The period antibute can be used in the prevention and treatment of
                                                                                                                                                                                                                                                                              R74333 standard; Protein; 514 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 95-067159/טץ.
N-PSDB; 084044.
Peptide antiallergic agent - inhibits cross-linking of allergen
                                                                                                                                                                                                                                                                                                                                                      182 IDIFASKNFHLQKNTIGTG 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MEIP ) MEIJI MILK PROD CO LTD. Kino K, Kohno Y, Komiyama N, WPI; 95-067159/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-JUL-1993; JP-177008.
01-SEP-1993; JP-217725.
07-APR-1994; JP-069336.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Japonicum sp. WO9502412-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antiallergic peptide; IgE cross-linking inhibition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Japonicum allergen residues 55-514, induced histamine release,
                                                                                                                                                                                                                                                                                                                                                                    31 IDIFASKNFHLQKNTIGTG 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R69791 standard; Protein; 460
R69791;
27-SEP-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               236 IDIFASKNFHLQKNTIGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31 IDIFASKNFHLQKNTIGTG 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
les 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       460 AA;
                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                514 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                         24.4%; Score 99;
100.0%; Pred. No.
tive 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24.4%; Su
100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entry)
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Pred. No.
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A
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                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; 1
. 2.1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Lo
                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 460;
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                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                      0;
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밁 Š RESULT
R53690
ID R53
AC R53
AC

Brauer A, WPI; 94-1

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RESULT 14
R81586
ID R81586
AC R81586
AC R81586
AC R81586
AC R81586
AC R81586
AC R81586
Cedar
KW Cedar
KW Cedar
KW Cedar
KW Cedar
KW Cedar
LOOK
COLUMN COLUMN
COLUMN
PR 14-JUI
PR
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RESULT 15
R93599
ID R93599
AC R93599
DT 16-MUG
DE Japan
KW Sujlerg
KW Sujlerg
KW Sujlerg
Cryptc
FH Key
FT peptic
FT protes
PN J0804:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PR 13-MAR-1995; 306295.

PR 10-SEP-1994; PP-242137.

PR 10-SEP-1995; JP-200221.

PR 14-JUL-1995; JP-200221.

PR 14-JUL-195; JP-200221.

PR 14-JUL-1995; JP-200221.

PR 14-JUL-1995; JP-200221.

PR 14-JUL-1995; JP-200221.

PR 14-JUL-195; JP-200221.

PR 14-JUL-1995; JP-200221.

PR 14-J
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The gene encoding an allergen of Japanese cedar pollen was isolated by PCR amplification using primers based on portions of the allergen protein. The gene was used for recombinant allergen production in E. coli (vector plasmid pKK-223-3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R81586 standard; Protein; 514 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cryptomeria japonica.
EP-700929-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R81586;
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                                                                                                                                                                                                                                         16-AUG-1996 (first entry)
Japan cedar pollen Cry j II allergen.
Allergen: epitope: overlapping peptide;
Sugi pollinosis; diagnosis; treatment.
                                                                                                                                                                                                                                                                                                                                             R93599 standard; Protein; 514 AA.
R93599;
16-AUG-1996 (first entry)
                                                                                                                                         peptide
                                                                      protein
                                                                                                                                                                                                                   Cryptomeria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31 IDIFASKNEHLQKNTIGTG 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
les 19; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                   japonica
                                        /*label= sig_peptide
55. .514
/*label= mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24.48; but
100.08; Pr
                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24.4%; >--
100.0%; Pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 99;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Le
2.5e-05;
                                                                                                                                                                                                                                                                                                    Cry j II; cedar pollen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 514;
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J08047392-A.

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20-FEB-1996;
07-NOV-1994; 297840.
05-NOV-1993; JP-276773.
05-MAY-1994; JP-134868.
26-MAY-1994; MILK PROD CO LTD.
(MEIF ) MEIGEA9/17.
N-PSDB; T18102.
                                                                 Japan cedar pollen allergen Cry j II epitope - comprises at least part of specified 460 amino acid protein

Claim 1; Page 10-11; 17pp; Japanese.

Claim 1; Page 10-11; 17pp; Japanese.

In the diagnosis, prevention and treatment of Sugi pollinosis, in the diagnosis, prevention and treatment of Sugi pollinosis, of the allergic reaction to Japan cedar pollen. Significant regions of the allergic reaction to Japan cedar pollen. Significant regions of the allergic reaction to Japan cedar pollen. Significant regions of the allergen were identified using overlapping peptides of the full epitope derived from a Cry j II antigen-specific T cell line epitope derived from a Cry j II antigen-specific T cell line of the full mature 460 amino acid allergen are the most allergenic of the 90 peptides tested.
                                                  Sequence
                                                            peptides tested.
514 AA;
DB 1;
  Length 514;
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Matches Query Match 236 IDIFASKNEHLOKNTIGTG 254 31 IDIFASKNFHLQKNTIGTG 49 Local Similarity 100. les 19; Conservative 24.4%; Score 99; 100.0%; Pred. No. 0; Mismatches 2.5e-05; Gaps

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search completed:
Job time: 2050 sec September 29, 1999, 13:35:10

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us-09-142-524-1.rpr

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4 3 2 H
                                                       PIR_60:*
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Copyright (c) 1993 - 1998 Compugen Ltd.
pir2:*
pir3:*
pir4:*
                                         pir1:*
                                                                                     40065486 residues
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result

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236 IDIFASKNEHLOKNTIGTG 254

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616 379 167 994 1163 215
222222
JC4084 S55845 B23093 A47474 S07137 A48463
prolyl endopeptida 3-isopropylmalate glycogen phosphory NAD+ ADP-ribosyltr DNA-directed RNA p Ras-like GTP-bindi

### ALIGNMENTS

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R:Namba, M.; Kurose, M.; Torigoe, K.; Hino, K.; Taniguchi, Y.; Fukuda, S.; Usui, M.; FEBS Lett. 353, 124-128, 1994
A;Title: Molecular cloning of the second major allergen, Cry j II, from Japanese ceda A;Reference number: S48730; MUID:95010777
A;Accession: S48730;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Cryptomeria japonica (Japanese cedar)
C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jul-1995
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A; Residues: 1-514 < NAM>
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A; Mesidues: 52-61 < MO2>
A; Residues: 52-61 < MO2>
R; Sakaguchi, M.; Inouye, S.; Taniai, M.; Ando, S.; Usui, M.; Matuhasi, T.
R; Sakaguchi, M.; Inouye, S.; Taniai, M.; Ando, S.; Usui, M.; Matuhasi, T.
A; Hergy 45, 309-312, 1990
A; Hergy 45, 309-312, 1990
A; Hergy 45, 309-312, 1990
A; Hergy 45, Molecular and Mo
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A;Accession: PC2346
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A; Residues: 1-514 <KOM>
                                                                                                                                                                                                                                                                                                            A;Molecule type: protein
A;Residues: 55-64 <SAK>
A;Residues: 55-64 <SAK>
C;Reywords: glycoprotein; pollen
F;1-54/Domain: signal sequence #status predicted <SIG>
F;1-54/Domain: second major allergen Cry j #status predicted <MAT>
F;429,460,472/Binding site: carbohydrate (Asn) (covalent) #status predicted
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31 IDIFASKNFHLOKNTIGTG 49
                                                                                                                             Local Similarity
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tive 0; Mismatches 0;
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C; Date: 31-Mar-1992
C; Accession: JH0419
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A; Molecule type: protein
A; Residues: 22-53;58-81;219-232;236-258;299-307;346-372 <SO2>
A; Residues: 22-53;58-81;219-232;236-258;299-307;346-372 <SO2>
A; Note: the authors described carbohydrate binding site for residue 279
C; Keywords: glycoprotein; pollen
C; Keywords: glycoprotein; pollen
F; 12-1/Domain: signal sequence #status predicted <SIG>
F; 12-1/Domain: signal sequence #status predicted <SIG>
F; 12-3/4/Product: major allergen Cry j I (clone pCCI-2-2) #status predicted <MAT
F; 158, 191, 293, 354/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                            ribosomal protein S18, cytosolic - rat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:D26544; NID:g493631; PID:d1006086; PID:g493832
A;Experimental source: pollen
A;Accession: PC2065
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A; Residues: 1-374 < SON>
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F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-374/Product: major allergen Cry j I (clone pCCI-15) #status predicted <MAT>
F:158,191,293,354/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A;Title: Cloning and sequencing of cDNA coding for Cry j I, a major allergen of Japanese A;Reference number: JC2123; MUID:94183234
A;Accession: JC2124
A;Accession: JC2124
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A;Experimental source: pollen
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R;Vladimirov, S.N.; Ivanov, A.V.; Karpova, G.G.; Musolyamov, A.K.; Egorov, T.A.; Thie Eur. J. Biochem. 239, 144-149, 1996
A;Title: Characterization of the human small-ribosomal-subunit proteins by N-terminal A;Reference number: S68931; MUID:96305378
A;Mccession: S68935
A;Mclecule type: protein
A;Residues: 'S',56-57,'X',59-64,'XX',67-69 <VLA>
                                                                                                                                                                                                                                                                             A;Cross-references: GDB:138447; OMIM:180473
A;Map position: 6p21.3-6p21.3
C;Superfamily: Escherichia coli ribosomal protein S13
C;Keywords: blocked amino end; protein biosynthesis; ribosome
                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: GDB: RPS18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Feb-1999
R;Chassin, D.; Bellet, D.; Koman, A.
Nucleic Acids Res. 21, 745, 1993
A;Title: The human homolog of ribosomal protein S18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-152 < CHA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Chan, Y.L.; Paz, V.; Wool, I.G.
Blochem. Biophys. Res. Commun. 178, 1212-1218, 1991
A;Title: The primary structure of rat ribosomal protein S18.
A;Reference number: JH0419; MUID:91337062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-152 < CHA>
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60 TEDEVERVITIMQNPRQYK 78
                                         62 ASRRVDGIIAAYQNPASWK 80
                                                                                                                12 PNRRVFIKRVSNVIIHGRRIDIFASKNFHLOKNTIGTGRR-----ISLKLTSGKI 61
                                                                    6 PEKFQHILRVLNTNIDGRRKIAFAITAIK-----GVGRRYAHVVLRKADIDLTKRAGEL 59
                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                 17.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17.2%;
                                                                                                                                                                           7; Mismatches
                                                                                                                                                                                       Score 70; DB 2; Length 152; Pred. No. 0.33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 152;
).33;
                                                                                                                                                                 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32; Indels
                                                                                                                                                                    16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16;
                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2:
```

1/0000 ribosomal protein S13 - mouse C;Species: Mus musculus (house mouse) C;Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 05-Feb-1999 C·Accession: I76666; IS7006

RESULT

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R;MacMurray, A.J.; Shin, H.S.
Mamm. Genome 2, 87-95, 1992
A;Title: The murine MHC encodes a mammalian homolog of bacterial ribosomal protein S13.
A;Reference number: I57006; MUID:92182530
A;Accession: I76666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A:Residues: 1-103, 'H', 105-152 <RE2>
A:Cross-references: GB:M'6762; NID:g198577; PID:g198578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:M76763; NID:g198579; PID:g198580
A;Accession: I57006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-152 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Introns: 1/3; 34/3; 97/3; 128/2
C; Superfamily: Escherichia coli ribosomal protein S13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable membrane protein YMR118c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YM9718.17c
N;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 08-Jul-1995 #sequence_revision 19-Oct-1995 #text_change 21-Nov-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: S54580
R;Hunt, S.; Bowman, S.
submitted to the EMBL Data Library, May 1995
A;Reference number: S54510
A;Accession: S54580
A;Accession: DNA
A;Molecule type: DNA
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Cross-references: EMBL:Z49702; NID:g817859; PID:g817878; MIPS:YMR118c
A,Experimental source: strain AB972
C:Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                      A;Map position: 13R
C:Keywords: transmembrane protein
F;98-114/Domain: transmembrane #status predicted <TM1>
F;179-195/Domain: transmembrane #status predicted <TM2
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sensory transduction histidine kinase sll1590 - Synechocystis sp. (strain PCC 6803) N;Alternate names: protein sll1590 C;Species: Synechocystis sp.
                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 PNRRVEIKRVSNVIIHGRRIDIFASKNFHLQKNTIGTGRR-----ISLKLTSGKI 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 TEDEVERVITIMONPROYK 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 ASRRVDGIIAAYQNPASWK 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 PEKFQHILRVLNTNIDGRRKIAFAITAIK-----GVGRRYAHVVLRKADIDLTKRAGEL 59
                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                          49 GRRISLKLISGKIASRRVDGIIAAYQNPASW 79
                                                                                                                                                    59 SNKEEELLVSOR-KKRPISPHLTVYEPEMSW 88
                                                                                                                                                                                                                                     1 MKATIORVTSVEGVPRASVEVPRISTPEILHNYISNG-RMDLE-SKEFHNGRVSKSDLWS 58
                                                                                                                                                                                                                                                                           1 MKVTV--AENOFG-PNRRVFIKRVS-----NVIIHGRRIDIFASKNFH---LQKNTIGT 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S54580
                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17.2%;
                                                                                                                                                                                                                                                                                          16.4%; but No. 29.7%; pred. No. 29.7%; pred. No. 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 70; DB 2
Pred. No. 0.33;
                                                                                                                                                                                                                                                                                                                                                Score 66.5; DB 2; Length 196; Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                      predicted <TM2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32;
                                                                                                                                                                                                                                                                                                                                       33; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                7;
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A; Variety: PCC 6803
C; Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 21-Aug-1998
C; Accession: S75065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; Kaneko, T.; Sato,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:D90910; GB:AB001339; NID:g1652956; PID:d1018660; PID:g165301
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-350 <KAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: S74322; MUID: 97061201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Start codon: GTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 glycoprotein E precursor - turkey herpesvirus N;Alternate names: ORF 8 protein C;Species: turkey herpesvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-498 <ZEL>
A;Residues: 9lycoprotein; transmembrane protein
C;Keywords: 9lycoprotein; transmembrane predicted <SIG>
F;1-18/Domain; signal sequence #status predicted <MAT>
F;19-498/Product: 9lycoprotein E #status predicted <TMM>
F;396-412/Domain: transmembrane #status predicted <TMM>
F;344,60,133,148,370/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Title: The complete sequence and gene organization of the short unique region of A,Reference number: JQ2346
A,Accession: JQ2353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 09-Sep-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasana, Res. 3, 109-136, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R; Zelnik, V.; Darteil, R.; Audonnet, J.C.; Smith, G.D.; Riviere, M.; Pastorek, J.;
                                                                                                                                                                                                               probable transport protein yejW - Reclinomonas americana (ATCC 50394) mitochondric (Species: mitochondrion Reclinomonas americana A, Variety: ATCC 50394 A, Variety: ATCC 50394 #sequence_revision 06-Feb-1998 #text_change 17-Mar-1999 C; Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 17-Mar-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                   R;Lang, B.F.; Burger, G.; O'Kelly, C.J.; Cedergren, R.; Golding, G.B.; Lemieux, C. Nature 387, 493-497, 1997
Nature 387, 493-497, 1997
A;Title: An ancestral mitochondrial DNA resembling a eubacterial genome in miniatory. Reference number: $78127; MUID:97311393
A;Accession: $78174
A; Molecule type: DNA
                            A; Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         246 QRVFNNLITNAINHSPRGRKVEISLTSKNNHFQVQIVDEGRGI 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 39.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 RRVFIKRVSNVIIH---GRRIDI-FASKNFHLQKNTIGTGRRI 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   y Match 16.0%; Score 65; DB 2; Length 498; Local Similarity 31.6%; Pred. No. 4.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                    92 ILRVDREVVNSGSLDRIASSQFHYIPNVIIGTGRGKELTIFN---ATSQIAGVYTRY 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 IKRVSNVIIHGRRIDIFASKNFHLQKNT-IGTGRRISLKLTSGKIASRRVDGIIAAY 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 66; I
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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A; Residues: 1-222 <LAN>

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pectate lyase - trumpet lily
C; Species: Lilium longiflorum (trumpet lily)
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                                                                   S29612
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C;Superfamily: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase II; 1-phosphati hodiesterase domain Y homology; pleckstrin repeat homology; SH2 homology; SH3 homology C:Keywords: phosphoproted in; phosphoric diester hydrolase
F; 322-464/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X homology
F; 550-657/Domain: SH2 homology CSH21>
F; 668-756/Domain: SH2 homology CSH21>
F; 798-846/Domain: SH3 homology CSH3>
                                                                                                                                                                                                                                                                                                                                                                  F;952-1073/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain y hd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GDB:120299; OMIM:172420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        *; Gene: GDB: PLCG1; PLC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:M34667; NID:9190037; PID:9190038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-1290 <BUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mol. Cell. Blol. 10, 4770-4777, 1990
A:Title: Characterization and cDNA cloning of phospholipase C-gamma, a major substrate f
A:Reference number: A36466; MUID:90355993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase (EC 3.1.4.11) - human C:Species: Homo sapiens (man) C:Date: 15-Feb-1991 #sequence_revision 15-Feb-1991 #text_change 12-Feb-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a; status:
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F;24-209/Domain: ATP-binding cassette homology <ABC>
F;41-48/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Genome: mitochondrion
G;Function:
A;Cerunction: involved in cytochrome c1 biosynthesis
C;Superfamily: cytochrome c biogenesis protein CycV; !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A:Cross-references: EMBL:AF007261; NID:g2258325; PID:g2258373
A:Experimental source: ATCC 50394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: yejw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                            943 MERR 946
                                                                                                                                                                                            883 IAIRPEGKNNRLEVFSISMASVAHWSLDVAADSQEELQDWVKKIREVAQTADARLTEGKI 942
                                                                                                                                                                               62 ASRR 65
                                                                                   13
                                                                                                                                                                                                                                   5 VAFNQEGPNRRVFIKRVSNVIIHGRRIDIFASKNFHLQ---KNTIGTGRRISLKLTSGKI 61
                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 GDIII 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 VDGII 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 IKRVSNVIIH---GRRID--IFASKNEHLOKNTI-----GTGRRISLKLTSGKIASRR 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 LTKIQNLTIHNTTGIRSNKIIFQNINFSLEKGSLFIIQGSNGSGKTTLLKIISGLLPKSQ 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             preliminary
                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20;
                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                    15.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15.8%; Score 64; DB 30.8%; Pred. No. 2.5;

 9; Mismatches

                                                                                                                                                                                                                                                                                                                Score 62.5;
Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                      DB 2; Length 1290;
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                                                                                                                                                                                                                                                                                      34;
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A;Gene: papE; prsE
C;Superfamily: papE fimbrial protein
C;Keywords: fimbria; pili adhesion
F;1-24/Domain: signal sequence #statu
                                                                                                                                 A;Cross references: EMBL:x61238; NID:g42526; PID:g42527
A;Experimental source: strain J96
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1991
C;Comment: This protein is one of the minor components of pili. Pili with a defective
                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:M13239; NID:g147074; PID:g147075
R;Marklund, B.I.; Tennent, J.M.; Garcia, E.; Hamers, A.; Baga, M.; Lindberg, F.; Gaas Mol. Microbiol. 6, 2225-2242, 1992
A;Title: Horizontal gene transfer of the Escherichia coli pap and prs pili operons as A;Reference number: S25205; MUID:93023852
                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-173 <MA2>
                                                                                                                                                                                                                                                                                                   A;Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:x61239; NID:g42290; PID:g42299
A;Experimental source: strain J96
                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-173 <MAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-173 <LUN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A:Cross-references: EMBL:M13239; NID:g147074; PID:g147075
R:Lund, B.; Lindberg, F.; Normark, S.
J. Bacteriol. 170, 1887-1894, 1988
A:Title: Structure and antigenic properties of the tip-located P pilus proteins of ur A:Reference number: A27743; MUID:88169520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Lindberg, F.; Lund, B.; Normark, S.
Proc. Natl. Acad. Sci. U.S.A. 83, 1891-1895, 1986
A;Title: Gene products specifying adhesion of uropathogenic Escherichia coli are mino.
A;Reference number: A25134; MUID:86149403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-173 <LIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Escherichia coli
C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 29-May-1998
C;Accession: A25134; A27743; S25222; S25227; S16401; S16406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N; Alternate names:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-434 < KIM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: S29611
A; Accession: S29612
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52 ISLKLTSGKIASRRVDGIIAAYQNPASW 79
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  sequence #status predicted <SIG>
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28.4%; Pred. No. 7.9;
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RESULT 15
S62737
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C:Species: Thermotoga maritima
C:Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C:Accession: S62737
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                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-633 <BOU>
A;Cross-references: EMBL:U27841; NID:g881493; PID:g881494
C;Superfamily: DNA topoisomerase I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Bouthier de la Tour, C.; Kaltoum, H.; Portemer, C.; Confalonieri, F.; Hubert, R.; Dugu Blochim. Biophys. Acta 1264, 279-283, 1995
A;Title: Cloning and sequencing of the gene coding for topoisomerase I from the extremel A;Reference number: S62737; MUID:96138548
A;Accession: S62737; MUID:96138548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 15.3%; Score 62; DB 1; Length 173; Best Local Similarity 27.0%; pred. No. 3.3; Matches 20; Conservative 11; Mismatches 35; Indels 8; Gaps
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search completed: September 29, 1999, 13:35:51 Job time: 2091 sec
                                                                                                                                                                                                                                                                                                                    Ouery Match 15.1%; Score 61.5; DB 2; Length 633; Best Local Similarity 25.4%; Pred. No. 16; Matches 16; Conservative 14; Mismatches 32; Indels 1; Gaps
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                                                                                                                          155 LWR 157
                                                                                                                                                                                                                                                                       18 IKRVSNVIIHGRRIDIFASKNFHLQKNTIGTGRRISLKLTSGKIASRRVDGIIAAYQNPA 77
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54.5 54

13.4 13.3

PPCK\_ANASU ASA1\_ENTFA

009460 anaerobiosp P17953 enterococcu

GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 29, 1999, 13:14:01; Search time 21.98 Seconds (without alignments) 102.887 Million cell updates/sec

Title:
Perfect score:
Sequence:

US-09-142-524-1 406 1 MKVTVAFNQFGPNRRVFIKR.....IASRRVDGIIAAYQNPASWK 80

Scoring table: BLOSUM62

Searched: 77977 seqs, 28268293 residues

SwissProt\_37:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

42 43	40 41	39	38	3 G	35	34	33	32	<b>ω</b>	30	29	) ·	3 4 6	: 13	24	20	22	21	20	19	1 1 7	17	15	14	13	12	11	10	οα	7	o	σ	4	ω	2	ш	No.	Result	
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RESULT 1  WRALCHIAN  IN MARCH 1995 (REL. 32, CREATED)  PROFESSION STANDARD; PRT; \$14 AA.  AC 193212;  AC 1932 (REL. 32, CREATED)  TO 1. MOV 1995 (REL. 33, LAST SMOKATION UDBATE)  TO 1. MOV 1995 (REL. 35, LAST SMOKATION UDBATE)  TO 1. MOV 1995 (REL. 35, LAST SMOKATION UDBATE)  PROFESSION FOR THE PROFESSION OF THE PROPERTY.  CONTROLLEN ALLERGER CRY J 2) (RRY J 11).  CS CRYPORERIA ANDROUGH (ADMINISCEDAR).  CC EUFMANDARY VIRIDIFLANTAR; STREPTOHYTA, EMERYOPHYTA; FRACHEOPHYTA, COLIFERALES;  TANDIACAR; CRYPORERIA.  RE SALUME FROM N.A., AND PARTIAL SEQUENCE.  RE VIRIDIFLANTAR; STREPTOHYTA, EMERYOPHYTA; FRACHEOPHYTA, COLIFERALES;  TANDIACAR; CRYPORERIA.  RE VIRIDIFLANTAR; STREPTOHYTA, EMERYOPHYTA; FRACHEOPHYTA, COLIFERALES;  TANDIACAR; CRYPORERIA.  RE VIRIDIFLANTAR; STREPTOHYTA, EMERYOPHYTA; FRACHEOPHYTA, COLIFERALES;  REALIES, SALUMER; STREPTOHYTA, COLIFERALES;  RE VIRIDIFLANTAR; STREPTOHYTA, EMERYOPHYTA; FRACHEOPHYTA, EMERYOPHYTA, EMPORENCE CEDATE, EMERYOPHYTA, EME
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RESULT 2
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Best Local S
Matches 19
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P18632;
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EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; CONIFEROPSIDA; CONIFE
                                                                           HIJIKATA A., MATSUMOTO I., KOJIMA K., OGAWA H.;

"Antigenicity of the oligosaccharide molety of the Japanese cedar
(Cryptomeria japonica) pollen allergen, Cry jI.";

INT. ARCH. ALLERGY IMMUNOL. 105:198-202(1994).

-i- PTM: CONTAINS FUCOSE/XYLOSE-CONTAINING FULNKED OLIGOSACCHARIDES.

-i- DISEASE: THIS PROTEIN IS THE MAJOR ALLERGEN OF JAPANESE CEDAR
POLLEN, THE MOST COMMON POLLEN ALLERGEN IN JAPAN.

-i- THE SEQUENCE OF CRY J I FORM A IS SHOWN HERE. FORM B DIFFERS IN
                                                                                                                                                                                                                                                                                                                                                                       "Cloning and sequencing of cDNA coding for Cry j I, of Japanese cedar pollen."; BIOCHEM. BIOCHYS. RES. COMMUN. 199:619-625(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1990 (REL. 16, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
SUGI BASIC PROTEIN PRECURSOR (SBP) (MAJOR ALLERGEN CRY J 1) (CRY J
This SWISS-PROT entry is copyright. It is produced through a continuous the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
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                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                           SIMILARITY: BELONGS TO THE AMB A I/AMB A II/CRY J I SI
                                                                     SIX POSITIONS.
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ilarity 100.0%;
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                                            SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          *****
                                                         POLYSACCHARIDE LYASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               467F3F33
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K (IN REF. 2).

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R (IN REF. 2).

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J. 0.00023;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A
                                                                                                                                                                                                                                                      SAKAGUCHI M., INOUYE S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONIFERALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 514;
                                                         FAMILY
                                                                                                                                                                                                                                  of Japanese cedar
                                                                                                                                                                                                                                                                                                                                                                                              a major allergen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRACHEOPHYTA;
 restrictions
         a collaboration - MBL outstation -
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RS18_
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Best Local S
Matches 15
                                                                                                                                                                                                                                                                                                                                        01-MAY-1992 (REL. 22, C
01-MAY-1992 (REL. 22, L
01-NOV-1997 (REL. 35, L
40S RIBOSOMAL PROTEIN S
                                                                                                                                                                                                          MEDLINE; 93181276.
CHASSIN D., BELLET I
"The human homolog on NUCLEIC ACIDS RES.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                    RS18_HUMAN P25232;
                                                                                                                                                                                                                                                                                                                                                                                                           _HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARIANT
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; D26544; G493632;
EMBL; D26545; G493634;
EMBL; D34639; G516728;
PIR; A44773; A44773.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
            SEQUENCE FROM N.A. SPECIES=PIG;
                                                                                                                                                      SPECIES=RAT; STRAIN=SPRAGUE-DAWLEY; TISSUE=LIVER; MEDLINE; 91337062.
CHAN Y.-L., PAZ V., WOOL I.G.;
                                                                                                                                                                                                                                                                                              HOMO SAPIENS (HUMAN), RATTUS NORVEGICUS (RAT), MUS MUSCULUS (MOUSE), AND SUS SCROFA (PIG).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
                                                     MACMURRAY A.J., SHIN H.S.;
"The murine MHC encodes a protein S13.";
                                                                                                                                  BIOCHEM. BIOPHYS.
                                                                                                                                                                                                                                                      SPECIES-HUMAN;
                                                                                                                                                                                                                                                                                      PRIMATES; CATARRHINI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIGNAL
KIMURA M., KAWAKAMI K.,
                                            MAMM. GENOME
                                                                                       MEDLINE; 92182530
                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                              "The
                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     234 MKVTVAFNQFGPNCGQRMPRARYGLVH 260
                                                                                                                                primary structure of rat ribosomal protein S18 HEM. BIOPHYS. RES. COMMUN. 178:1212-1218(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MKVTVAFNQFGPNRRVFIKRVSNVIIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O544; pec_lyase; GLYCOPROTEIN; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                           2:87-95(1992)
                                                                                                                                                                                                                                                     TISSUE=PLACENTA;
                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                        22, CREATED)
22, LAST SEQUENCE UPDATE)
35, LAST ANNOTATION UPDAT
TEIN S18 (KE-3) (KE3).
                                                                                                                                                                                                          D., KOMAN A.;
of ribosomal protein
21:745-745(1993).
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143
202
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221
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                                                                                                                                                                                                                                                                                      HOMINIDAE;
  SUZUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MULTIGENE FAMILY;
                                                                 mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MW;
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L -> Y (IN
S -> T (IN
L -> S (IN
C -> H (IN
FOTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 71; DB 1
Pred. No. 0.35;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
DC088629
 H., HAMASIMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             I BASIC PROTEIN.

F (IN CRY J 1-B).

Y (IN CRY J 1-B).

T (IN CRY J 1-B).

I (IN CRY J 1-B).

H (IN CRY J 1-B).

H (IN CRY J 1-B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27
                                                                homolog
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                                                                                                                                                                                                                                                                                                                                                     UPDATE !
                                                                                                                                                                                                                     S18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRC32;
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  z
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                                                                of bacterial ribosomal
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X57529; G433447; -.
EMBL; X69150; -; NOT_ANNOTATEC
EMBL; M76763; G198580; -.
EMBL; M76762; G198578; -.
EMBL; AB000911; G1841304; -.
PIR; JH0419; R3RT18.
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                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
PUTATIVE SUCCINATE DEHYDROGENASE CYTOCHROME B
YMR118C OR YM9718.17C.
                                                                                                                                                                                                   HUNT S., BOWMAN S., BARRELL B.G., RAJANDREAM M.A.;
SUBMITTED (MAY-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- FUNCTION: MONO-HEME CYTOCHROME B. INVOLVED IN SYSTEM II OF THE
MITOCHONDRIAL ELECTRON TRANSPORT CHAIN WHICH IS RESPONSIBLE FOR
                                                                                                                                                                                                                                                                                                                                        SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               YM07_YEAST
Q04487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RIBOSOMAL PROTEIN.
RIBOSOMAL PROTEIN.
104
104
177 AA; 17719 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBMITTED (FEB-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- FUNCTION: INVOLVED IN THE BINDING OF FMET-TRNA AND, HENCE, IN INITIATION OF TRANSLATION (BY SIMILARITY).
                                                                                                                 -!- SIMILARITY: BELONGS TO THE CYTOCHROME B560 FAMILY.
                                                                                                                                                                                                                                                                            STRAIN-S288C / AB972;
                                                                                                                                                                                                                                                                                                                               SACCHAROMYCETACEAE;
                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: BELONGS TO THE S13P FAMILY OF RIBOSOMAL PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60
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                                                                                                                                                 (BY SIMILARITY).
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
                                                                                                                                                                        TRANSFERRING ELECTRONS FROM SUCCINATE TO UBIQUINONE (COENZYME (BY SIMILARITY).
                                                                                                                                      INNER MEMBRANE (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TEDEVERVITIMONPROYK 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PNRRVFIKRVSNVIIHGRRIDIFASKNFHLQKNTIGTGRR-----ISLKLTSGKI 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JH0419;
S30393;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ASRRVDGIIAAYQNPASWK 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PEKFQHILRVLNTNIDGRRKIAFAITAIK-----GVGRRYAHVVLRKADIDLTKRAGEL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGI:98146; RPS18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
requires a license agreement (See http://www.isb-sib.ch/announce,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS00646; RIBOSOMAL_S13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S30393.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                            SACCHAROMYCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -> H (IN G198578).
F215ADD4 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 196 AA.
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0.17;
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                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                   EMBL outstation
                                                                                 a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16;
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                 commercial
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RESULT 5
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Best Local
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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TRANSMEM
SEQUENCE
                                                                                                                                                                                               EMBL; Z17328; G19451; -. EMBL; L18911; G308902; -. PIR; S29612; S29612.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KIM S.R., FINKEL D.J., AN G.;
SUBMITTED (JUN-1993) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- CATALYTIC ACTIVITY: ELIMINATIVE CLEAVAGE OF PECTATE TO GIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PEL_LILLO P40973;
                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LILIUM LONGIFLORUM (TRUMPET LILY).
EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; LILIOPSIDA; LILIALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UF
15-DEC-1998 (REL. 37, LAST ANNOTATION
PECTATE LYASE PRECURSOR (EC 4.2.2.2).
                                                  CARBOHYD
                                                                                                    CHAIN
                                                                                                                                                                                    PFAM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=CV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS01000; SDH_CYT_1; 1.

PROSITE; PS01001; SDH_CYT_2; 1.

PFAM; PF01127; Sdh_CYT_1.

HYPOTHETICAL PROTEIN; TRICARBOXYLIC ACID CYCLE;

HYPOTHETICAL PROTEIN; MITOCHONDRION; TRANSIC PEPT

MEMBE; TRANSMEMBRANE; MITOCHONDRION; TRANSIC PEPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LILIACEAE; LILIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49 GRRISLKLTSGKIASRRVDGIIAAYQNPASW 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 SNKEEELLVSQR-KKRPISPHLTVYEPEMSW 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                               SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OLIGOSACCHARIDES WITH 4-DEOXY-ALPHA-D-MANN-4-ENURONOSYL GROUPS AT THEIR NON-REDUCING ENDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MKATIQRVTSVFGVPRASVFVPRISTPFILHNYISNG-RMDLF-SKEFHNGRVSKSDLWS
                                                                                                                                                                    PF00544; pec_lyase;
                                                                                                                                                       SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NELLIE WHITE; TISSUE=POLLEN;
                          1
23
312
68
97
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175
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  AA;
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31, LAST SEQUENCE UPDATE)
37, LAST ANNOTATION UPDATE)
- - - - - - - - - - - - 2 2).
                          434
312
68
97
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  48457
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29.7%;
MW;
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                                             PECTATE LYASE.
POTENTIAL.
POTENTIAL.
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POTENTIAL.
2C868EA3
                                                                                                                          POTENTIAL
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PUTATIVE SUCCINATE DEHYDROGENASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C6610BB3 CRC32;
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CRC32;
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIP4_HUMAN
P19174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7TLBERSTEIN A., SCHLESSINGER J., JAYE M.;
"h=>=0; etalion and cDNA cloning of phospholipase C-gamma, a m-
substrate for heparin-binding growth factor 1 (acidic fibroblast
growth factor)-activated tyrosine kinase.";
MOL. CELL. BIOL. 10:4770-4777(1990).
use by non-profit institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                       CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
1-PHOSPHATIDYLINOSITOL-4,5-BISSPORSPHATE PHOSPHODIESTERASE GAMM (EC 3.1.4.11) (PLC-GAMMA-1) (PHOSPHOLIPASE C-GAMMA-1) (PLC-II)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 90355993.
BURGESS W.H., DIONNE C.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLCG1 OR PLC1.
HOMO SAPIENS (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BRIDGEMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIMATES; CATARRHINI; HOMINIDAE;
                                                                                                               This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IISSUE=VEIN, AND BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCHLESSINGER J., INAGAKI F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRUCTURE BY NMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBMITTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Solution structure of the SH3 domain of phospholipase C-gamma."
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                                                                                                                                                                                                                     SYSTEM RECEPTORS.

THERE ARE AT LEAST SIX FORMS OF PLC ENZYMES.

CTMTTARTTY: DOMAINS X AND Y ARE CONSERVED IN DIFFERENT FORMS

CTMTTARTTY: DOMAINS X AND Y ARE CONSERVED ACTIVITY.
                                                                                                                                                                                                                                                                                                                                       TYROSINE KINASE.

CATALYTIC ACTIVITY: 1-PHOSPHATIDYL-D-MYO-INOSITOL 4,5-BISPHOSPHATE + H(2)O = D-MYO-INOSITOL 1,4,5-TRIPHOSPHATE + DIACYGLYCEROL.

COFACTOR: REQUIRES CALCIUM.
                                                                              s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                            OF PLC AND ARE ESSENTIAL FOR CATALYTIC SIMILARITY: CONTAINS 1 C2 DOMAIN. SIMILARITY: CONTAINS 2 PH DOMAINS. THE
                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: PLC-GAMMA IS A MAJOR SUBSTRATE FOR HEPARIN-BINDING GROWTH FACTOR 1 (ACIDIC FIBROBLAST GROWTH FACTOR)-ACTIVATED
                                                                                                                                             SIMILARITY: CONTAINS SIMILARITY: CONTAINS
                                                                                                                                                                                                                                                                                                            PTM: THE RECEPTOR-MEDIATED ACTIVATION OF PLC-GAMMA INVOLVES THEIR PHOSPHORYLATION BY TYROSINE KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MQYTVAFNHFGRGLVQRMPRCRYGFVHVVNNDYTHWIMYAVGGSQH----PTIISQGNRY 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MKVTVAFNQFGPN-----RRVFIKRVSNVIIHGRRIDIFASKNFHLQKNTIGTGRR- 52
                                                                                                                                                                                                                                                                                           TO LIGATION OF A VARIETY OF GROWTH FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IAPHIEAAKEVTKR-----DYAEPAEW 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (JUL-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OF SH3 DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11;
                                                                                                                                             SH2 DOMAINS.
SH3 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KAPLOW J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 4.2;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERTEBRATA; MAMMALIA;
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                                                                                                                                                                                                                                                                                             AND IMMUNE
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YPI2_AGRT6
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Best Local
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DOMAIN 27
CA_BIND 165
DOMAIN 320
DOMAIN 489
DOMAIN 550
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ACT_SITE
ACT_SITE
MOD_RES
MOD_RES
MOD_RES
SEQUENCE
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DOMAIN
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                                    SEQUENCE
MEDLINE;
KANEMOTO
                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50001; SH2; 2.
PROSITE; PS50002; SH3; 1.
PROSITE; PS50003; PH_DOMAIN;
PROSITE; PS50004; C2_DOMAIN_;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
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MEDIINE: 89213933.
KRANEMOTO R.H., POWELL A.T., AKIYOSHI D.E., KERSTETTER R.A., NESTER E.W., HAWES M.C., RESTERTER E. A.C., HAWES M.C., Tom Agrobacterium tumefaciens.";
J. BACTERIOL. 171:2506-2512(1989).
                                                                                                             01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UF
01-NOV-1997 (REL. 35, LAST ANNOTATION
HYPOTHETICAL 15.8 KD PROTEIN IN PINF2
                                                                                                                                       Q44433;
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFAM; PF00388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFAM;
                                                                                           PLASMID PTIA6
                                                                                                   AGROBACTERIUM TUMEFACIENS.
                                                                                                                                                           YPI2_AGRT6
                                                                          RHIZOBIACEAE; AGROBACTERIUM
                                                                                                                                                                                                      943 MERR 946
                                                                                                                                                                                                                                          883 IAIRPEGKNNRLFVFSISMASVAHWSLDVAADSQEELQDWVKKIREVAQTADARLTEGKI
                                                                                                                                                                                                                        62 ASRR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L; AL022394; E13121; A36466; A36466.; 2HSP; 31-AUG-94.; 1HSQ; 31-AUG-94.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; PF00017; SH2;
; PF00018; SH3;
; PF00168; C2; 1
                                                                                                                                                                                                                                                          VAFNQFGPNRRVFIKRVSNVIIHGRRIDIFASKNFHLQ---KNTIGTGRRISLKLTSGKI 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M34667; G190038;
                                                                                                                                                                                                                                                                                       Similarity
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PS50007;
                                                        FROM N.A.
                                                                                                                                                                                                                         65
                                                                                   PROTEOBACTERIA; ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIPID DEGRADATION;
                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                           STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHOSPHORYLATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C2_DOMAIN_2; 1.
PIPLC_X_DOMAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIPLC_Y_DOMAIN;
                                                                                                                                                                                                                                                                                                                                    1253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                _DOMAIN; 2.
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Pred. No. 14;
9; Mismatches
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BY SIMILARITY.
BY SIMILARITY.
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SH2.
SH3.
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DOMAIN Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
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                                                                                   SUBDIVISION;
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                                                                                                                                                                                                                                                                                       NO. 14;
                                                                                                                                 UPDATE
                                     D.E.,
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                                                                                                              UPDATE)
                    plant-inducible locus
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                             GORDON M.P.
                                                                                                                                                                                                                                                                              34;
                                                                                     RHIZOBIACEAE GROUP;
                                                                                                                                                                                                                                                                                                <u>;</u>
                                                                                                              (ORF2).
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( SIMILARITY).
( SIMILARITY).
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                                     D.A.,
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1988
01-AUG-1988
15-DEC-1998
                                                                                             MARKLUND B.-I., TENNENT J.M., GARCIA E., HAMERS A., BAGA M.,
LINDBERG F., GAASTRA W., NORMARK S.;
"Horizontal gene transfer of the Escherichia coli pap and prs pili
operons as a mechanism for the development of tissue-specific
adhesive properties.";
MCL. MICROBIOL. 6:2225-2242(1992).

MICROBIOL. 5:2225-2242(1992).

-i. FUNCTION: FINERIAE (ALSO CALLED PILI), POLAR FILAMENTS RADIATING
FROM THE SURFACE OF THE BACTERIUM TO A LENGTH OF 0.5-1.5
MICROMETERS AND NUMBERING 100-300 PER CELL, ENABLE BACTERIA TO
COLONIZE THE EPITHELIUM OF SPECIFIC HOST ORGANS.

-i. FUNCTION: THIS PROTEIN IS ONE OF THE MINOR COMPONENTS OF PILI.
PILLI WITH A DEFECTIVE PAPE GENE WILL HAVE LOW ADMESSIVE CAPACITY
PILLI WITH A DEFECTIVE PAPE GENE WILL HAVE LOW ADMESSIVE CAPACITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/pr send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 88169520.

LUND B., LINDBERG F., NORMARK S.;

"Structure and antigenic properties of the tip-located proteins of uropathogenic Escherichia coli.";

J. BACTERIOL. 170:1887-1894(1988).
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HYPOTHETICAL PROTEIN; PLAS
SEQUENCE 145 AA; 15829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LINDBERG F., LUND B., NORMARK S.;
"Gene products specifying adhesion of uropathogenic Escherichia coli are minor components of pili.";
PROC. NATL. ACAD. SCI. U.S.A. 83:1891-1895(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1988 (REL. 08, CREATED)
01-AUG-1988 (REL. 08, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDAT
FIMBRIAL PROTEIN PAPE PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION;
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SUBCELLULAR LOCATION: SECRETED;
DISEASE: STRAINS OF E.COLI THAT
URLNARY TRACT PRODUCE PAP-PILL
CONSISTING OF ABOUT 1000 HELICAL
                                                                                  OR NONE; HOWEVER,
                                                                  BE AFFECTED
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17; Conser
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INS OF E.COLI THAT CAUSE INFECTION OF THE HUMAN PRODUCE PAP-PILI WHICH ARE HAIR-LIKE APPENDAGE. ABOUT 1000 HELICALLY ARRANGED SUBUNITS OF THE
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5829 MW;
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Pred. No. 1
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RESULT 9
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Best Local (
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EMBL; M13239; G147075; -.

EMBL; M20146; G147090; -.

EMBL; X61239; G42299; -.

PIR; A25134; YOECPE.
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modified
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01-NOV-1995 (REL.
01-OCT-1996 (REL.
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                                                                               the
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STRAIN-MSB8
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                                                                                                         between
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                                                                                                                                                                                                                                                                                            MITTED (MAY-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.

FUNCTION: THE REACTION CATALYZED BY TOPOISOMERASES LEADS TO THE CONVERSION OF ONE TOPOLOGICAL ISOMER OF DNA TO ANOTHER. CATALYZIC ACTIVITY: AFF-INDEPENDENT BREAKAGE OF SINGLE-STRANDED DNA, FOLLOWED BY PASSAGE AND REJOINING.

SUBUNIT: MONOMER (BY SIMILARITY).

WHEN A TOPOISOMERASE TRANSIENTLY BREAKS A DNA BACKBONE BOND, IT WHEN A TOPOISOMERASE TRANSIENTLY BREAKS A DNA BACKBONE BOND, IT
                                                                            European
                                                                                                                                                                                                     SIMILARITY: BELONGS TO PROKARYOTIC TYPE I/III TOPOISOMERASE
                                                                                                                                                                                                                                                   SIMULTANEOUSLY FORMS A PROTEIN-DNA LINK, IN IN THE ENZYME IS JOINED TO A DNA PHOSPHORUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LINE THE URINARY TRACT.
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CONTAINING GLYCOLIPIDS PRESENT ON THE EPITHELIAL CELLS WHICH
                                                                                                                                                                                                                                 ENZYME-SEVERED DNA STRAND
                                                                     SWISS-PROT entry is copyright. It is produced through a collaboratic een the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on it
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pean Bioinformatics Institute. There are no restrictions on its non-profit institutions as long as its content is in no way and this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FROM N.A.
SB8 / DSM 3109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THERMOTOGALES; THERMOTOGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32, CREATED)
32, LAST SEQUENCE UPDATE)
34, LAST ANNOTATION UPDATE)
1 (EC 5.99.1.2) (OMEGA-PROTEIN) (RELAXING ENZYME)
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27.0%;
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Best Local S
Matches 16
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Best Local 9
                                                                                                                                                                                  FLYBASE; FBgn0010411; RpS18.
PROSITE; PS00646; RIBOSOMAL_S13; 1.
PFAM; PF00416; S13; 1.
                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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                                                                                                                                                                                                                                                                                                                                                                                       "The Drosophila melanogaster homolog of ribosomal protein S18.", GENE 141:231-235(1994).
-!- FUNCTION: INVOLVED IN THE BINDING OF FMET-TRNA AND, HENCE, INTITIATION OF TRANSLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RS18_DROME STANDARD; PRT; 152 AA P41094; PREL. 31, CREATED) 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE) 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDAT
                                                                                                                                                            RIBOSOMAL PROTEIN. SEQUENCE 152 AA;
                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GARWOOD J., LEPESANT J.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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PTERYGOTA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DROME
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PROSITE; PS00396; TOPOISOMERASE_I_PROK;
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                                                                                                                                                                                                                                                                                                                                                                           INITIATION OF TRANSLATION (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE S13P FAMILY OF RIBOSOMAL PROTEINS.
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59 GKIASRRVDGIIAAYQNPASWK
                                                      12 PNRRVFIKRVSNVIIHGRR---IDIFASKNFHLQKNTIGTGRR-----ISLKLTS 58
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                              σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RIBOSOMAL PROTEIN S18.
                            PEKFQHILRIMNTNIDGKRKVGIAMTAIK--
                                                                                                                                                                                                                                 L22959; G349256; -
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                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MELANOGASTER (FRUIT FLY).
METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSE
DIFTERA; BRACHYCERA; MUSCOMORPHA; EPHYDROIDEA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOISOMERASE; DNA-BINDING.
288 288 DNA CLEAV
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                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              288 1
72694 MW;
                                                                                                                                                          17611 MW;
                                                                                                 15.0%;
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                                                                                    10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 61.5; DI
Pred. No. 8.5;
14; Mismatches
 08
                                                                                                 Score 61;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FLY).
; TRACHEATA; HEXAPODA; INSECTA;
                                                                                                                                                         72CA0DCB CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9C0D9F68 CRC32;
                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLEAVAGE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   152 AA.
                                                                                                             DB 1;
                            --GVGRRYSNIVLKKADVDLTKRA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32;
                                                                                    29;
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                                                                                                             Length 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 633;
                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                      HENCE, IN
                                                                                  22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
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RESULT 11
Y12K_SMSV4
В
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PHS2_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                  MEDITIE: 86248098.

OSAWA S., CHIU R.H., McDoNOUGH A., Mosolation of partial cDNAs for rat phosphorylase isozymes.";
FEBS LETT. 202:282-288(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-1994 (REL. 29, CREATED)
01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
POSSIBLE 12 KD NUCLEIC ACID-BINDING PROTEIN.
SAN MIGUEL SEA LION VIRUS (SEROTYPE 4) (SMSV 4).
VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Y12K_SMSV4
P36289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-1989 (REL. 10, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-CCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
MEDLINE; 86030264.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLYCOGEN PHOSPHORYLASE, MUSCLE FORM (EC 2.4.1.1) (MYOPHOSPHORYLASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P09812;
                                                                                                                                                                                                                                                                            SUBMITTED
                                                                                                                                                                                                                                                                                                      SEQUENCE OF 2-842 FROM N.A. HUDSON J.W., HEFFERON K.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                    EUKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                           RATTUS NORVEGICUS (RAT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PHS2_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M87482; G334889; -. PIR; D48562; D48562.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Nucleotide sequence of the capsid protein gene of two serotypes san Miguel sea lion virus: identification of conserved and non-conserved andno acid sequences among calicivirus capsid proteins. VIRUS RES. 24:211-222(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE; 92410750.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CALICIVIRUS
                          SEQUENCE OF 763-842 FROM N.A.
                                                                                                                                                                                                                   SEQUENCE OF 566-762 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NEILL J.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: TO FELINE CALICIVIRUS 12 KD PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 FLNSVANAVVEGKKLDL-ASKGLQLKSRALDTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 FIKRVSNVIIHGRRIDIFASKNFHLQKNTIGTGR 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h 14.9%;
Similarity 32.4%;
11; Conservative 1
                                                                                                                                                                                                                                                                            (OCT-1993)
                                                                                                                                                                                                                                                                                                                                                                                       SCIUROGNATHI; MURIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                    METAZOA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     110 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                     CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; THI; MURIDAE; MURINAE; RATTUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12566 MW;
                                                                                                                                                                                                                                                                          TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10;
                                                                                                                                                                                                                                                                                                      CRERAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 60.5;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                     MILLER
t liver
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12;
                                                                                                                                  . JR., JOHNSON G.L.;
muscle glycogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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RESULT 13
FKH2_YEAST
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Best Local S
Matches 22
                                                                                                                                                                                                                                                          CONFLICT
CONFLICT
CONFLICT
SEQUENCE
       FKH2_YEAST STANDARD; PRT; 862 AA. P41813; O1-NOV-1995 (REL. 32, CREATED) O1-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE) 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                    SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Comparative sequence analysis of rat, rabbit, and human muscle glycogen phosphorylase cDNAs."; EUR. J. BIOCHEM. 152:267-274(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                  BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L10669; G204423; -. EMBL; X03032; G818028; -.
                                                                                                                                                                                                                                                                                                       BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; B24200; B24200.
PIR; C23093; C23093.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute.
FORK HEAD PROTEIN HOMOLOG 2.
                                                                                                                                                                                                                                                                                                                              ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSFERASE; GLYCOSYLTRANSFERASE; CARBOHYDRATE METABOLISM;
GLYCOGEN METABOLISM; ALLOSTERIC ENZYME; PYRIDOXAL PHOSPHATE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CRERAR M.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HWANG P.K.,
                                                                                                              811
                                                                                                                                                         751
                                                                                                                                    60
                                                                                                                                                                               10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COFACTOR: PYRIDOXAL PHÓSPHATE.
SUBUNIT: HOMODIMER. DIMERS ASSOCIATE INTO A TETRÁMER TO FORM
ENZYMATICALLY ACTIVE PHOSPHORYLASE A.
SIMILARITY: BELONGS TO THE GLYCOGEN PHOSPHORYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: PHOSPHORYLASE IS AN IMPORTANT ALLOSTERIC ENZYME IN CARBOHYDRATE METABOLISM. ENZYMES FROM DIFFERENT SOURCES DIFFER IN THEIR REGULATORY MECHANISMS AND IN THEIR NATURAL SUBSTRATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATALYTIC ACTIVITY: (1,4-ALPHA-D-GLUCOSYL)(N) (1,4-ALPHA-D-GLUCOSYL)(N-1) + ALPHA-D-GLUCOSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROPERTIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                              KFSS---DRTIAQY 821
                                                                                                                                   KIASRRVDGIIAAY
                                                                                                                                                        FSPKQPDLFKDIVNMVMHHDRFKVFADYEEYIKCQDKVSELYKNPREWTRMVIRNIATSG 810
                                                                                                                                                                            FGPNRRVFIKRVSNVIIHGRRIDIFA-----SKNFHLQKNTIGTGRRISLKL-TSG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PF00343; phosphorylase; P00489; 1PYG.
                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS00102; PHOSPHORYLASE;
                                                                                                                                                                                                                                                                                 681
640
724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEE Y.P., VINCENTINI A.M., POWERS M.A., FLETTERICK R.J.,
                                                                                                                                                                                                                                                                                                                                                   143
                                                                                                                                                                                                                                                                                                                                                                           109
                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                              156
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                                                                                                                                                                                                                                                                                                                                                                                                76
                                                                                                                                                                                                                                                             AA;
                                                                                                                                                                                                                                                         766
97273 MW;
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641
724
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                                                                                                                                                                                                                                                                                                                                                                                                                       15
                                                                                                                                                                                                             14.78;
29.78;
                                                                                                                                                                                                   Score 59.5; D
Pred. No. 20;
9; Mismatches
                                                                                                                                                                                                    9;
                                                                                                                                                                                                                                                        MAY BE INVOLVED IN THE ALLOSTERIC CONTROL OF ENTRME ACTIVITY (BY SIMILARITY).

PYRIDOXAL PHOSPHATE (BY SIMILARITY).

RF -> L (IN REF. 2).
Q -> N (IN REF. 2).
V -> L (IN REF. 3).
V -> L (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                              INVOLVED IN THE ASSOCIATION OF (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                    MAY BE INVOLVED IN SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                           PHOSPHORYLATION (BY PHK) (CONVERTS PHOSPHORYLASE B TO A).
                                                                                                                                                                                                                                                                                                                                          (BY
                                                                                                                                                                                                                                                                                                                                                  INVOLVED IN THE ASSOCIATION
                                                                                                                                                                                                                                                                                                                                        SIMILARITY).
                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                    30;
                                                                                                                                                                                                                                                                                                                                                                                               AMP
                                                                                                                                                                                                                         Length 842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                + ORTHOPHOS
                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                               (BY
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Best Local
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SUBMITTED (XXX-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 96021608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=S288C / FY1676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of six ORFs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 97060022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YEAST 12:391-402(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                             PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ERRATUM
                             69
                                                                                                         Local
                                                    71
                                                                        11 GPNRRVFIKRVSNVIIHGRRIDIFASKNFHLQKNTIG--TGRRISLKLTSGKIASRRVDG
        IIKYNMNIGGWE 136
                             IIAAYQNPASWK 80
                                                    GPNWTYYVKDLEVSI--GRNTD---PLNSALQENSDGVKNSYRVNIDLGPAKVVSRK-HA 124
                                                                                                          Similarity
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EMBL; L38850; G623608; -...
EMBL; X86470; G791119; -...
EMBL; Z71343; E328836; -...
EMBL; Z71344; E328903; -...
EMBL; U11141; G1098481; -...
SGD; L0002608; FKH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BERGEZ P., DOIGNON F., CROUZET M.;
YEAST 12:297-297(1996).
-i- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
-i- SIMILARITY: CONTAINS 1 FORK-HEAD DOMAIN.
-i- SIMILARITY: CONTAINS 1 FHA DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chromosome XIV from Saccharomyces cerevisiae.";
YEAST 11:967-974(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BERGEZ P., DOIGNON F., CROUZET M.; "The sequence of a 44 420 bp fragment located on the left arm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     reveals 12 new open reading frames (ORFs) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FKH2 OR YNL068C OR N2403 OR YNL2403C.
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)
                                                                                                                                           PFAM; PF00498; FHA; 1.
DNA-BINDING; NUCLEAR PROTEIN.
DOMAIN 83 152
DNA_BIND 339 430
SEQUENCE 862 AA; 94374 MW;
                                                                                                                                                                                                                                                                                                           PROSITE; PS00657; FORK_HEAD_1; 1.
PROSITE; PS00658; FORK_HEAD_2; 1.
PROSITE; PS50006; FHA_DOMAIN; 1.
PROSITE; PS50039; FORK_HEAD_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-440 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POEHLMANN R., PHILIPPSEN P.;
"Sequencing a cosmid clone of Saccharomyces cerevisiae chromosome XIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SACCHAROMYCETACEAE; SACCHAROMYCES.
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                                                                                                                                                                                                                                                      PF00250; Fork_head; 1. PF00498; FHA; 1.
     Conservative
                                                                                                                                           430 FORK-HEAD.
94374 MW; 83DA8394 CRC32;
                          14.5%;
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  11;
                          Score 59;
Pred. No.
     Mismatches
                             DB 1;
24;
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                                                        Length 862;
  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                PASCAL S.M., SINGER A.U., GISH G., YAMAZAKI T., SHOELSON S.E., PAWSON T., KAY L.E., FORMAN-KAY J.D.; PAWSON T. MAY L.E., FORMAN-KAY J.D.; SHOELSON S.E., PAWSON T., KAY L.E., FORMAN-KAY J.C., FO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIP4_BOVIN
P08487;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "PDGF stimulation of inositol phospholipid hydrolysis requires PLC-gamma 1 phosphorylation on tyrosine residues 783 and 1254."; CELL 65:435-441(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 91208680.
KIM H.K., KIM J.W., ZILBERSTEIN A., MARGOLIS SCHLESSINGER J., RHEE S.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. BIOL.
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                                                                                                                                                                                                                                                                                                                             -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. BIOL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NATURE 332:269-272(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND MEDLINE; 88156963.
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01-AUG-1988 (REL. 08, LAST SEQUENCE UPDATE)
101-AUG-1988 (REL. 36, LAST ANNOTATION UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHOLIPASE C-GAMMA-1) (PLC-II)
(EC 3.1.4.11) (PLC-GAMMA-1) (PHOSPHOLIPASE C-GAMMA-1) (PLC-II)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1988 (REL.
01-AUG-1988 (REL.
15-JUL-1998 (REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Tyrosine residues in bovine phospholipase C-gamma
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                                           THERE ARE AT LEAST SIX FORMS OF PLC ENZYMES. SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN OF PLC AND ARE ESSENTIAL FOR CAMALYTIC ACTIVISIMILARITY: CONTAINS 1 C2 DOMAIN.

SIMILARITY: CONTAINS 2 PH DOMAINS. THE SECONE
                                                                                                                                                                      + H(2)O = D-MYO-INOSITOL 1,4,5-TRIPHOSPHATE + DIACYGLYCEROL.
COPACTOR: REQUIRES CALCIUM.
PTM: THE RECEPTOR-MEDIATED ACTIVATION OF PLC-GAMMA 1 AND 2
INVOLVES THEIR PHOSPHORYLATION BY TYROSINE KINASES IN RESPONSE
TO LIGATION OF A VARIETY OF GROWTH FACTOR RECEPTORS AND IMMUNE
SYSTEM RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAURUS (BOVINE).

ARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES
DIACYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS
MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE
                                                                                                                                                                                                                                                                                                            CATALYTIC ACTIVITY: 1-PHOSPHATIDYL-D-MYO-INOSITOL 4,5-BISPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                epidermal
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CONTAINS 2 SH2 DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             factor receptor in
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with the non-catalytic region
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                                                   SECOND ONE
                                                                                                 ACTIVITY
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Matches 17
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PROSITE: PSS0001; SH2; 2.
PROSITE: PSS0002; SH3; 1.
PROSITE: PSS0003; PL_DOMAIN;
PROSITE: PSS0004; C2_DOMAIN;
PROSITE: PSS0004; C2_DOMAIN;
PROSITE: PSS0008; PIPIC_X_DO
PROSITE: PSS0008; PIPIC_Y_DO
PROM; PF00017; SH2; 2.
PFAM; PF00018; C2; 1.
PFAM; PF0018; C2; 1.
PFAM; PF0018; C2; 1.
PFAM; PF0018; PH; 2.
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                                                  YSP3_YEAST STANDARD; PRT; 478 AA P25036; 01-MAY-1992 (REL. 22, CREATED) 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE) 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDAT SUBTILISIN-LIKE PROTEASE III PRECURSOR (EC YSP3 OR YOR003W.
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PROSITE;
           SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES;
SACCHAROMYCETACEAE; SACCHAROMYCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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2PLD; 26-JAN-95.
2PLE; 26-JAN-95.
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                                                                                                                                                                                                                                                                      VAFNQFGPNRRVFIKRVSNVIIHGRRIDIFASKNFHLQ---KNTIGTGRRISLKLTSGKI
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PI-PLC-X; 1.
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; PIPLC_X_DOMAIN;
; PIPLC_Y_DOMAIN;
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Pred. No. 43;
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DOMAIN Y.
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                                                              UPDATE)
R (EC 3.4.
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                           SACCHAROMYCETALES;
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"The sequence of a 30 kb fragment on the left arm of chromosome XV from Saccharomyces cerevisiae reveals 15 open reading frames, five which correspond to previously identified genes.";
YEAST 12:1091-1095(1996).
-I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PFAM; PF00082; subtilase; 1. HSSP; P06873; 3PRK. HYDROLASE; SERINE PROTEASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00136; SUBTILASE_ASP; 1. PROSITE; PS00137; SUBTILASE_HIS; 1. PROSITE; PS00138; SUBTILASE_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M77197; G173237; -. EMBL; U43491; G1150998; -. EMBL; Z74911; E252316; -. SGD; L0002552; YSP3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration in the EMBL outstation of Bioinformatics and the EMBL outstation of the Laropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MASON O.B., WONG P.A., BARR P.J.;
SUBMITTED (XXX-1991) TO EMBL/GENBANK/DDBJ DATA BANKS.
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SUBTILISIN-LIKE PROTEASE III.
SUBTILISIN-LIKE PROTEASE III.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
D -> E (IN REF. 1).
N -> D (IN REF. 1).
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MISSING (IN REF. 1).
Y -> L (IN REF. 1).
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Pred. No. 14;
14; Mismatches
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GenCore version 4.5

Copyright (c) 1993 - 1998 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 29, 1999, 13:02:00; Search time 45:11 Seconds (without alignments)

Perfect score: 406
Sequence: US-09-142-524-1
Perfect score: 406
Sequence: 1 MKVTVAFNOFGPNRRVFIKR.....IASRRVDGIIAAYQNPASWK 80

Scoring table: BLOSUM62
Searched: 201082 seqs, 61543640 residues

Database: SpTREMBL_10:*
1: Sp_archea:*
5: Sp_invertebrate:*
5: Sp_invertebrate:*
6: Sp_mammal:*
7: Sp_mhame:*
8: Sp_organelle:*
9: Sp_plant:*
11: Sp_rodent:*
12: Sp_vrtebrate:*
13: Sp_varchassified:*
14: Sp_unclassified:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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,	014926 homo sapien	009783 san miquel	O23017 arabidopsis	045758 caenorhabdi	CTOSES CARROTHEDAT	016342 030000000000000000000000000000000000	087960 borrelia hu	P74730 synechocyst	Q38355 lactococcus	COCTOZ SCHIZOSACCH	060100 5065 50000	09zan5 comamonas s	Q51714 pyrococcus	ATOMO CACIOTHADAT			PITELED TO THE LEGIS		051514 borrelia hij	P97350 mus musculu

# ALIGNMENTS

RESULT 2 09ZNU7  D7 09ZNU7  D8 09ZNU7  PRELIMINARY; PRT; 367 AA.  AC 09ZNU7;  D7 01-MAY-1999 (TREMBLrel. 10, Created) D7 01-MAY-1999 (TREMBLrel. 10, Last sequence update) D7 01-MAY-1999 (TREMBLrel. 10, Last annotation update) D7 01-MAY-1999 (TREMBLrel. 10, Last annotation update) D8 POLLEN MAJOR ALLERGEN 1-2. OS Juniperus ashei (Ozark white cedar). OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo; OC cuphyllophytes; Spermatophyta; Coniferopsida; Coniferales; RN [1]	Query Match Best Local Similarity 59.3%; Pred. No. 0.51; Matches 16; Conservative 2; Mismatches 9; Indels  QY 1 MKVTVAFNQFGPNRRVFIKRVSNVIIH 27	RELIMINARY; PRT; 375 AA.  ITEMBLICAL 02, Created) ITEMBLICAL 02, Last sequence update) ITEMBLICAL 02, Last sequence update) Obtusa.  Obtusa.  Spermatophyta; Coniferopsida; Coniferales; Chamaecyparis.  N.A.  1194.  N.A.  CHAMA N., ITOH M., ITOH H., SONE T., KUNO K.,  Characterization and molecular cloning of Chamaecyparis obtusa (Japanese cypress) pc BAA08246.1; - CHAOD:1088;1.  PEC_lyase; 1.  1 21 POTENTIAL. CHAOI. SAA; 40258 MW; A0981492 CRC32;
Tracheophyta;	); Gaps	Tracheophyta; trales; UNO K., TAKAGI I., g of Cha o 1, a ress) pollen.";
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           046197
046197;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Molecular cloning of mountain cedar (Juniperus ashei) pollen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-CANTON S; TISSUE-ACCESSORY GLAND; WOLFNER M.F., HARADA H.A., BERTRAM M.J., STELICK T.J., KRAUS KALB J.M., LUNG Y.O., NEUBAUM D.M., PARK M., TRAM U.; Insect Biochem. Mol. Biol. 27:0-0(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Arthropoda; Pterygota; Diptera; Brachycera;
                                                                                                                                                   065456;
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PFAM; PF00059; lectin_c; 1.
SEQUENCE 234 AA; 27173 MW; F674589C CRC32;
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                        Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                 PECTATE LYASE LIKE PROTEIN. F1N20.180.
                                                                                                           01-AUG-1998 (TIEMBLrel. 07, Created)
01-AUG-1998 (TIEMBLrel. 07, Last seq
01-MAY-1999 (TIEMBLrel. 10, Last ann
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nes 15; Conserv
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                                                                                                                                                                                                                                    NIQDEKELDGILALAPNNSYW 168
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Pred. No. 0.49;
9; Mismatches 3
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BEVAN M., WEDLER H., WAMBUTT R.,
SCHUELLER C.;
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Submitted (APR-1998) to the EM
EMBL; ALO22140; CAA18111 1; -
PFAM; PF00544; pec_lyase; 1.
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P73865;
01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-JAN-1999 (TREMBLREL. 09, Last annotation update)
SENSORY TRANSDUCTION HISTIDINE KINASE.
Synechocystis sp. (Strain PCC 8803).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y., MIYAAIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T., HOSOUCHI T., MATSUNO A., MURAKI A., NAKAZAKI N., NARUO K., OKUMURA SHIMPO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., YASUDA M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 68;
Pred. No.
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                                                                                                                                         Score 66; DB 2; Length 350; Pred. No. 4.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95399178 CRC32;
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                                                                                                               Mismatches
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                                                                                                                                       STRAIN=CV. COLUMBIA;
STRAIN=CV. COLUMBIA;
VYSOTSKAIA V.S., OSBORNE B.I., SCHWARTZ J.R., TORIUMI M., YU G.,
KWAN A., OJI O., LIU S., BUEHLER E., CONWAY A.B., CONWAY A.R.,
DEWAR K., FENG J., KIM C., KURTZ D., PALM C.J., LI Y., SHINN P.,
SUN H., DAVIS R.W., ECKER J.R., FEDERSPIEL N.A., THEOLOGIS A.;
SUBMITTED (MAY-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AC002131; AAC11625.1; -.
EMBL; AC002131; AAC11625.1; -.
EFAM; PF00544; Pec_lyase; 1.
FFAM; PF00544; Pec_lyase; 1.
                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1998 (TrEMBLrel 07, Created)
01-AUG-1998 (TrEMBLrel 07, Last seq
01-MAY-1999 (TrEMBLrel 10, Last anno
                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A
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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons;
enre endicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                           Arabidopsis.
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Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases
EMBL; AL022140; CAA18112.1; -.
PFAM; PF00544; pec_lyase; 1.
246 MRVTIAFNHFGPGLIERMPRVRRGYAHVANNRYEKWQMYAIGGSADPTIFSEGNYF---- 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
PECTATE LYASE LIKE PROTEIN.
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                               1 MKVTVAFNQFGPNRRVFIKRVSNVIIH-------GRRID--IFASKNFHLQKN 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45 TIGTGRRISLKLTSGKIASRRVDG 68
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                                                                                        Similarity
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                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                       16.0%;
                                                                     14;
                                                                  Score 65; DB 1
Pred. No. 6.2;
14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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Pred. No. 4.8;
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                                                                                                   DB 10; Length 390;
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                                                                     29;
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                                                                   Indels
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18 IKRVSNVIIH---GRRID--IFASKNFHLQKNTI------GTGRRISLKLTSGKIASRR 65

Matches Query Match Best Local

Local

Similarity

15.8%;

Score 64; DB | Pred. No. 4.1;

DB 8;

Length 222; Indels

Conservative

14; Mismatches

19;

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Q88525
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Best Local (
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O21280;
O1-JAN-1998 (TrEMBLrel. 05, C.
O1-JAN-1998 (TrEMBLrel. 08, L.
ATP-BINDING SUBUNIT OF ABC TR
LANG B.F., BURGER G.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF007261; AAD11907.1;
-FRAM; PF00005; ABC_tran; 1.
ATP-binding; Mitochondrion.
SEQUENCE 222 AA; 25502 MW; D81B02D7 CRC32;
                                                                                                                                                                                      STRAIN-ATCC50394;
                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 97311393.

LANG B.F., BURGER G., O'KELLY C.J., CEDERGREN R., GOLDING G.B.,
LEMIEUX C., SANKOFF D., TURMEL M., GRAY M.W.;
                                                                                                                                                                                                                                                                              Nature 387:493-497(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Reclinomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Reclinomonas americana.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The complete sequence and gene organization of the short unique region of herpesvirus of turkeys."; J. Gen. Virol. 74:2151-2162(1993).
EMBL: X68653; CAA48619.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q88525
Q88525;
                                                                                                                                                                                                                                                                                                                             An ancestral mitochondrial DNA resembling a eubacterial genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Turkey herpesvirus.
Viruses; dsDNA, viruses, no RNA stage; Herpesviridae.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
GLYCOPROTEIN HONOLOGUE E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZELNIK V., DARTEIL R., AUPASTOREK J., ROSS N.L.J.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
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18; Conservative
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, Last annotation update)
TRANSPORTER FOR CYTOCHROME
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RESULT
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01-JUN-1998 (TIEMBLEL. 06, Last sequence update)
01-JUN-1998 (TIEMBLIEL. 08, Last annotation update)
01-WOV-1998 (TIEMBLIEL. 08, Last annotation update)
HYPOTHETICAL 60.7 KD PROTEIN T19H12.1 IN CHROMOSOME V PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
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Hypothetical protein; Signal; Transmembrane.

SIGNAL 1 18 POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DAVIDSON S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
                                                                                                                                                         066004;
01-AUG-1998 (TrEMBLrel. 07, Created
01-AUG-1998 (TrEMBLrel. 07, Last so
01-AUG-1998 (TrEMBLrel. 07, Last an
MANNITOL-1-PHOSPHATE DEHYDROGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                      066004
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"Genetic and serological analysis of the immunogenic 67-kDa
lipoprotein of Mycoplasma sp. bovine group 7.";
Res. Microbiol. 149:55-64(1998).
                                    FREY J., CHENG X., MONNERAT M.-P., ABDO E.-M., KRAWINKLER M., BOLSKE G., NICOLET J.;
                                                                                                                        Mycoplasma bovine group 7.
Bacteria; Firmicutes; Bacillus/Clostridium
                                                           MEDLINE; 98439347.
                                                                         STRAIN-PG50
                                                                                      SEQUENCE FROM N.A.
                                                                                                           Mycoplasmataceae; Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63
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                                                                                                                                                                                                                                                                                 IINYY 78
                                                                                                                                                                                                                                                                                                         IIAAY 73
                                                                                                                                                                                                                                                                                                                                                                               19;
                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                        495
533 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                         AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                     18 1
533 1
172 1
280 E
515
60726 MW;
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                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                          Score 63.5;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
008AAF7D CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
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                                                                                                                         group; Mollicutes;
                                                                                                                                                                                                                                                                                                                                                                                17;
                                                                                                                                                                                                                                                                                                                                                                                                       Length 533;
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RESULT 12
Q47446
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                                                                                                                                                                                                                                                                                            Q15152 PRELIMINARY;
Q15152; 000645;
01-NOV-1996 (TrEMBLrel. 01, C
01-NOV-1996 (TrEMBLrel. 01, L
01-NOV-1998 (TrEMBLrel. 08, I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Structure and antigenic properties of the tip-located proteins of uropathogenic Escherichia coli.";
J. Bacteriol. 170:1887-1894(1988).
EMBL; M20181; AAA24291.; -.
PFAM; PF00419; Fimbrial; 1.
SEQUENCE 173 AA; 18450 MW; E09D027D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1998
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01-NOV-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE; 88169520.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria;
                                                                                                                                                                                                                     Homo sapiens (Human).
Homo sapiens (Human).
Thomas sapiens (Human).
Thomas sapiens (Human).
Thomas sapiens (Human).
                                                                                                                               [1]
SEQUENCE FROM N.A.
--- A . HANS H.W.,
                                                                                                                                                                                                           Eukaryota; Metazoa;
Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LUND B., LINDBERG F.,
Submitted (JUL-1994) to the
                                                                                        Submitted (JUL-1994) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                  PLAKOPHILIN
                        ZIMBELMANN R.
                                            SEQUENCE FROM N.A.
                                                                                                                   FRANKE W.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25 KYNISLNELNDYKIQIIKRLNNSFIKDDLKRLVRNTELKLSKN-----ERILTILDYAKV 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 ASRRVDGIIAAYQN 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 KIASRRVDGIIAAY 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93
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27.0%;
                                                                                                                                                                                                              Catarrhini;
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                                                                                                                                           SCHAEFER S.,
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Last annotation update)
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Pred. No. 3.
                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation updat
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Pred. No.
  EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                Hominidae;
                                                                                                                                              NUBER U.A.,
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                                                                                                                                                                                                                                                                                                           update)
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                                                                                                  databases
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                                                                                                                                                ZIMBELMANN
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AC 044584
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Q13835
ID Q13835
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DT 01-NOV
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OS HOMO S
OC EUKARY
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Best Local (
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Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                      044584;
01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
    STRAIN-BRISTOL N2;
MEDLINE; 94150718.
WILSON R., AINSCOU
                                                                                                                                                  Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
<sup>Bhahdirina:</sup> Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                  F48G7.4 PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Band 6 protein, a major constituent of desmosomes from stratified epithelia, is a novel member of the armadillo multigene family."; Cell Sci. 107:2259-2270(1994).

EMBL; X79293; CAR55881.1; -...

PFAM; PF00514; Armadillo_seg; 3.

SEQUENCE 725 AA; 80433 MW; 270BE242 CRC32;
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EMBL; Z34974; CAA84426.1; -.

EMBL; Z34974; CAA84822.1; -.

PFAM; PF00514; Armadillo_seg; 3.

SEQUENCE 726 AA; 80496 MW; A92E30E9 CRC32;
                                                                                                                                                                                                                                                                                                                                  F48G7.4
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HATZFELD M., KRISTJANSSON G.I., PLESSMANN U., WEBER K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 95074299.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-EPIDERMIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31 IDIFASKNFHLOKNTIGTGRRISLKLTSGKIASRRVDGI 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l Similarity
12; Conserv
AINSCOUGH R., ANDERSON K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Armadillo_seg; 3.
AA; 80433 MW; 270BE242 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.8%; Score 60; DB 30.8%; Pred. No. 52; tive 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              275 AA
    BAYNES C., BERKS M.,
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Best Local 9
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STRAIN-BRISTOL N2;

STRAIN-BRISTOL N2;

CLARKE K., WOHLDMANN P., HARRISON M.;

Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.

EMBL; AF03904; A[[47944.1]; -

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                                                                                         36 SKNFHLQKNTIGTGRRISLKLTSGKIASRRVDGII 70
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mes 12; Conserv
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                                                                                                                                                                                                                            14.8%;
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Pred. No. 16;
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AV239334 Homo sapiens mRNA for IgM H
I U37027 Sillago japonica repetit
AV239334 Homo sapiens mRNA for IgM H
I L26291 Caenorhabditis elegans
G28131 human STS SHGC-35660, se
I L22959 Drosophila melanogaster
U15448 Sus scrofa clone pvgl2a
X70203 H. Sapiens DNA for IgM he
X70204 H. Sapiens CMD mRNA for
Z33118 M. Cappicolum DNA for CON
X51510 Cappicolum DNA for CON
A51518 Sequence 3 from Patent
195550 Sequence 3 from patent
M93104 Saccharomyces cerevisia
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gb_pat:A67730
gb_sts:G48233
gb_ba1:ECOPAPEF
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Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
ID E09607 standard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: em_pat:E09607
                                                                                                                                      Sequence 1545 BP; 508 A; 283 C; 352 G; 402 T; 0 other;
                                                                                                                                                                                                                                                                                                                                      Nanba M., Torigoe K., Kurimoto M.;
"DNA CODING POLYPEPTIDE, RECOMBINANT DNA CONTAINING THE DNA AND
                                                                                                                                                                                                                                                                                                                                                          [1]
1-1545
                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA encoding polypeptide causing pollen allergy.
                                                                                  source
                                                                                                                                                                                                                                                                                                              Patent number JP 1995170986-A/1, 11-JUL-1995. HAYASHIBARA BIOCHEM LAB INC.
                                                                                                                                                                                                                                                                                                                                 TRANSFORMAT";
                                                                                                                                                                                                                                                                                                                                                                                     unidentified unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                              JP 1995170986-A/1.
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                                                                                                                                                                                                                            Cryptomeria (cedar)
p 1995170986-A/1
11-JUL-1995
20-DEC-1993 JP 1993344596
05-NOV-1993 JP 993 P 299151
NANBA MOTOJI, TORIGOE KAKUJI, KURIMOTO MASASHI
C12N15/09, C12N1/21, G01N33/50//A61K39/36, G01N33/53, G01N33/53, C12N1/21,
                                                                                                                              CDS
                                                                                                                                                        source
                                                                                                                                                                                           topology: Linear;
hypothetical: No;
                                                                                                                                                                                                            strandedness: Double;
                                                                                                                                                                                                                       C12R1:19);
                                                                                                                                                                                   anti-sense:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard; RNA; UNC; 1545 BP
                                                                                 1. .1545
                                                                                                  Location/Qualifiers
                                                              /organism="unidentified"
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                                                                                                                                                                                  No;
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52,
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58.00
62.00
                                                                                                                           /organism="Cryptomeria"
/tissue_type="pollen"
1. .1545
                                                                                                                 /product="polypeptide causing pollen allergy"
                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
Last updated, Version 1)
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87.47
87.52
Length:
Gaps:
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477 ! G48233 SHGC-60275 Human Homo
1284 ! M13239 E.coli papE and papF
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alignment\_block: US-09-142-524-1 x E09607

Percent Similarity:

Ratio:

5.211 100.000

Percent Identity:

100.000

0

Align seg 1/1 to: E09607

from: 1

to: 1545

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seq_documentation_block: ID E09664 standard
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US-09-142-524-1 x E09664
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                                                                                                    Quality: 99.00
Ratio: 5.211
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          756
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                                                                                                                                                                                                                                                                                                     Torigoe K., Nanba M., Kurimoto M.; "POLYPEPTIDE, ITS PRODUCTION AND USE"; Patent number JP 1995188289-A/1, 25-JUL-1995.
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1-1545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CUNA encoding a novel
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                                                                                                                                                                                         Sequence 1545 BP; 508 A; 281 C; 354 G; 402 T; 0 other;
                                                                                                                                                                                                                                                                           Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HAYASHIBARA BIOCHEM LAB INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unclassified.
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31 IleAspIlePheAlaSerLysAsnPheHisLeuGlnLysAsnThrIleGl 47
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                                                                                                                                                                                                                                                                                                                                                                                                                      25-JUL-1995
27-DEC-1993 JP 1993346814
TORICOE KAKUJI, NANBA MOTOJI, KURIMOTO MASASHI
CO7K14/415,A61K39/36,C12N15/09,C12P21/02,(C12P21/02,C12R1:19);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cryptomeria sp. JP 1995188289-A/1
                                                                                                                                                                                                                                                                                                                   SGS
                                                                                                                                                                                                                                                                                                                                                                                                                strandedness: Double;
                                                                                                                                                                                                                                                                                                                                                         source
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                                                                                                                                                                                                                                                                                                                                                                                                  Linear;
                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                     /db_xref="taxon:32644"
/organism="unidentified"
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52,
                                                                                                                                                                                                                                                .1545
                                                                                                                                                                                                                                                                                                                /organism="Cryptomeria sp."
/tissue_type="pollen"
1. .1545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last updated, Version 1)
                                                                                                                                                                                                                                                                                                   /product="hay fever-inducing protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein which induces hay fever.
                                                                                                                                                                                                                                                                                                                                                                                     location/Qualifiers
                                         from: 1
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                                                                                                         Gaps:
Percent Identity:
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REFERENCE
AUTHORS
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SOURCE
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LOCUS CPOCRYJII
                                                                                                                   BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  706 ATTGATATCTTTGCATCTAAAAACTTTCACTTACAAAAGAACACGATAGG 755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
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Cryptomeria japonica cDNA to mRNA.
Cryptomeria japonica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Komiyama, N., Sone, T., Shimizu, K., Morikubo, K. and Kino, cDNA cloning and expression of Cry j II, the second maj of Japanese cedar pollen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (02-AFR-1994) to the DDBJ/EMBL/GenBank databases. Naoki Komiyama, Meiji Institute of Health Science; 540 Naruda, Odawara, Kanagawa 250, Japan (Tel:0465-37-3661, Fax:0465-36-2776) (bases 1 to 1708)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Coniferopsida; Coniferales; Taxodiaceae; Cryptomeria.

1 (bases 1 to 1708)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Meiji Insitute of Health Science
540 Naruda, Odawara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Phone:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (02-Apr-1994) to DDBJ by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochemical and Biophysical Research Communication 201, 1021-1028
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/db_xref="GI: 550
                                                                                                                                                                                         GKIYHP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="allergen"
/protein_id="BAA06172.1"
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/db_xref="taxon:3369"
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alignment\_block:

Percent Similarity:

100.000

Percent Identity: 100.000

Length: Gaps:

Quality:

Ratio:

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99.00 5.211

US-09-142-524-1 x CPOCRYJII

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ID E10716 standard
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                                                                                                                                                                                                                                                Sequence 1733 BP; 593 A; 294 C; 380 G; 466 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sone T., Komiyama N., Kii K.;
"ALLERGEN CRY J II EPITOPE OF POLLEN OF JAPANESE CEDAR";
Patent number JP 199647392-A/1, 20-FEB-1996.
                                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-OCT-1997 (Rel. 52, Created) 08-OCT-1997 (Rel. 52, Last updated, Version 1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unclassified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA encoding cedar pollen allergen, Cryj2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               μ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       yThrGly 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTGATATCTTTGCATCTAAAAACTTTCACTTACAAAAGAACACGATAGG 799
                                                                                                                                                                             3'UTR
                                                                                                                                                                                                                            CDS
                                                                                                                                                                                                                                                                   mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sig_peptide
                                                                                                                                                                                                                                                                                                                                                           5'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           strandedness: Double;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             anti-sense: No;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical: No;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       topology:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard; RNA; UNC; 1733 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Linear;
                                                                                                                                 Location/Qualifiers
                                            /organism="unidentified"
                                                                   /db_xref="taxon:32644"
                                                                                          .1733
                                                                                                                                                                                                                                                                 /product="signal peptide of cedar pollen allergen, Cryj2" 207. .1586
                                                                                                                                                                                                                       /product="cedar pollen allergen,Cryj2"
45. .1589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                           /product="cedar pollen allergen,Cryj2"
1590. .1733
                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="Pollen"
                                                                                                                                                                                                                                                                                                                                                                                              'organism="Cryptomeria sp."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from: 1
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SOURCE
ORGANISM
          BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: gb_pl1:CPOCJIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: E10716 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-142-524-1 x E10716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 750 ATTGATATCTTTGCATCTAAAAACTTTCACTTACAAAAGAACACGATAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g577695
D37765.1 G1:577695
Cry j II; allergen.
Cryptomeria japonica pollen cDNA to mRNA.
Cryptomeria japonica
Cryptomeria japonica
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Coniferopsida; Coniferales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CPOCJIP 1790 bp mRNA
Cryptomeria japonica mRNA for Cry
D37765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Usui,M. and Kurimoto,M.
Molecular cloning of the second major allergen, Cry j II, from Japanese cedar pollen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (22-UUL-1994) to the DDBJ/EMBL/GenBank databases. Motoshi Namba, Fujisaki Institute, Hayashibara Biochemical Laboratories, Inc; Fujisaki 675-1, Okayama, Okayama 702, Japan (Tel:086-276-3141, Fax:086-278-6885)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Namba, M., Kurose, M., Torigoe, K., Hino, K., Taniguchi, Y., Fukuda, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Taxodiaceae; Cryptomeria.

1 (bases 1 to 1790)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Namba, M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lett. 353 (2), 124-128 (1994)
          ø
/ttanslation="MAKKF IAPMAFVAMOLIIMAAAEDOSAOIMLDSDIEQYLRSNRS
LRKVEHSRHDALMIFNVEKYGAVGDGKHDCTEAFSTAMQAACKRSAMLLVGOKKFVV
VNNLFFNGPOOPHFTFKVDGIIAAYONPASWKNNRIMLOFAKLIGFTLMGKGYLDGOG
KOWWAGOCKWVNOREICNDRDRFTAIKFDFSTGLIIQGLKLMNSPEFHLYGGNCEGVK
KIGISITAPRDSSNTDGJDIFASKNFHLOKNTIGTGDDCVALIGTGSSNIVIEDLIGG
GHGISIGSLGRENSRAEVSYVHVNGAKFIDDTOKLRIKTWQGGSGMASHIIYENVEMI
NSENPILLNOFYCTSASACQNORSAVQIODVTYKNIRGTSATAAAIOLKGDSMPKTUN
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GKIYHP"
325 c 392 4 488 t
                                                                                                                                                                                                                                                                   /product="Cry j II precur
/protein_ia="BAA07021.1"
/db_xref="PID:d1007598"
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/db_xref="GI:577696"
                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="pollen"
126. .1670
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Cryptomeria japonica"
/db_xref="taxon:3369"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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5.211
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                                                                                                                                                                                                                                                                                                                                                                II precursor"
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6
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ORIGIN

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alignment_block:
US-09-142-524-1 x CPOCJIP
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     seq_documentation_block:
ID E11677 standard
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Ratio: 5.211
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sone T., Komiyama N., Kii K.;
"ALLERGEN TO POLLEN OF CHAMAECYRARIS OBTUSA";
Patent number JP 1996176192-A/1, 09-JUL-1996.
MEIJI MILK PROD CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-OCT-1997 (Rel. 08-OCT-1997 (Rel.
                                                                                                                                                                                                                                                      THE FOR CONTRACTOR PROPERTY OF                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA encoding Cha o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       881 AACAGGG 887
Sequence 1062
                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JP 1996176192-A/1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1-1062
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chamaecyparis obtusa
pr 1996176192-A/1
09-JUL-1996 .
21-DEC-1994 JP 1994335089
SONE TOSHIO, KOMIYAMA NAOKI, KII KOUSUKE
SONE TOSHIO, KOMIYAMA NAOKI, KII KOUSUKE
                                                                                                                                                                                                                            mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                       strandedness: Double;
                                                                                                                                                                                                                                                                                                        source
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                                                                                                                                                                                                                                                                                                                                                                                  topology: Linear;
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     ВÞ;
                                                                                                 1. .1062
                                                                                                                                                     Location/Qualifiers
                                                    /organism="unidentified"
                                                                            /db_xref="taxon:32644"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52,
52,
  319 A; 198 C; 254 G; 291 T;
                                                                                                                                                                                                                            /organism="chamaecyparis obtusa"
/tissue_type="pollen"
1...1062
                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last updated, Version
                                                                                                                                                                                                    /product="Cha o I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
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Gaps: 0
Percent Identity: 100.000
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     0 other;
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seq_documentation_block:
ID E11678 standard;
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US-09-142-524-1 x E11677
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Ratio: 3.895
Percent Similarity: 70.370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sone T., Komiyama N., Kii K.;
"ALLERGEN TO POLLEN OF CHAMAECYRARIS OBTUSA";
Patent number JP 1996176192-A/2, 09-JUL-1996.
MEIJI MILK PROD CO LTD.
                                                                                                                                                                                                                                                                                                                                                               08-OCT-1997 (Rel. 08-OCT-1997 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                         d1110015
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        687 AATGCCAAGGGCACGATATGGACTTATACAT 717
                                                                    unclassified.
                                                                                                                                                                                                                                                                                                            unidentified
                                                                                                                                                                                                                                                                                                                             JP 1996176192-A/2.
                                                                                                                                                                                                                                                                                                                                              cDNA encoding Cha o I
                                 source
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                                                                                                                                                                                                                                                                          -1125
                                                                                                                                                                 Chamaecyparis obtusa
JP 1996176192-A/2
09-JUL-1996
21-DEC-1994 JP 1994335089
SONE TOSHIO, KOMIYAMA NAOKI, KII KOUSUKE
CO7K14/415,C12N15/09,C12P21/02//A61K35/12,A61K35/64,A61K35/72,
A61K35/74,
                                                                                    sig_peptide
                                                                           mat_peptide
                                                                                                               source
                                                                                                                                                 strandedness: Double;
                                                                                                                                                          A61K35/78, A61K39/36;
                                                                                                                                Key
                                                                                                                                       topology: Linear;
               1. .1125
/db_xref="taxon:32644"
/organism="unidentified"
                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                               52,
                                                                                                                                                                                                                                                                                                                                                                                                                                              RNA;
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/tissue_type="pollen"
1. .63
64. .1125
                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                               Created)
Last updated,
                                                                                                                                                                                                                                                                                                                                              precursor
                                                                    /product="Cha o I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                              UNC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length: 27
Gaps: 0
Percent Identity: 59.259
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                                                                                                                                                                                                                                                                                                                                                                Version
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Sequence 1125 BP; 327 A; 211 C; 264 G; 323 T; 0 other;

50. .112 113. .117

SSNPTILSEGNSFTAPNDSDKKEVTRRVGCESPSTCANWVWRSTQDSFNNGAYFVSSG KNEGTNIYNNNEAFKVENGSAAPQLTKNAGVLTCILSKPCS"

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REFERENCE
AUTHORS
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AUTHORS
TITLE
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    Quality:
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Ratio: 3.895
Percent Similarity: 70.370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Suzuki,M., Komiyama,N., Itoh,M., Itoh,H., Sone,T., Kino,K., Takagi,I. and Ohta,N.
Purification, characterization and molecular cloning of Cha o 1, a major allergen of Chamaecyparis obtusa (Japanese cypress) pollen Mol. Immunol. 33 (4-5), 451-460 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chamaecyparis obtusa male pollen cDNA to mRNA, clone:pCH-1. Chamaecyparis obtusa Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Coniferopsida; Coniferales; cupressaceae; Chamaecyparis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (31-JAN-1995) to the DDBJ/EMBL/GenBank databases. Toshio Sone, Meiji Institute of Health Science, Department of Pharmaceutical Research; 540 Naruda, Odawara, Kanagawa 250, Japan (Tel:0465-37-3661, Fax:0465-36-2776)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chao1
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D45404.1 GI:1514942
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Product="Chaol"

product="Fichaol"

product="Fichaol"

protein_id="Baa08246.1"

protein_id="Baa08246.1"

/db_xref="pl0:q1514943"

/db_xref="gl:1514943"

/db_xref="gl:151494"

/db_xref="gl:151494"

/db_xref="gl:151494"

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/db_xref="g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Chao1"
50. .1177
                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                /function="allergen"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="pCH-1"
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/db_xref="taxon:13415"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="pollen"
l. .1256
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Gaps: 0
Percent Identity: 59.259
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alignment_block:
US-09-142-524-1 x D45404
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        PRESENTATION OF PRESENTATION O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sone T., Komiyama N., Kii K.;
"ALLERGEN TO POLLEN OF CHAMAECYRARIS OBTUSA";
Patent number JP 1996176192-A/3, 09-JUL-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEIJI MILK PROD CO LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unidentified
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     sig_peptide
                                                        CDS
                                                                                                                                   source
                                                                                                                                                                                                                                                                                              SONE TOSHIO, KOMIYAMA NAOKI, KII KOUSUKE
C07K14/415,C12N15/09,C12P21/02//A61K35/12,A61K35/64,A61K35/72,
                                                                                                                                                                                                                                                                                                                                              09-JUL-1996
21-DEC-1994 JP 1994335089
                                                                                                                                                                                                                                                                                                                                                                                                         Chamaecyparis obtusa JP 1996176192-A/3
                                                                                                                                                                                     Key
                                                                                                                                                                                                                                strandedness: Double;
                                                                                                                                                                                                                                                        A61K35/78, A61K39/36;
                                                                                                                                                                                                           :opology: Linear;
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233 c 282
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52, Last upd
/organism="Chamaecyparis obtusa"
/tissue_type="pollen"
50. .1177
/product="Cha o I precursor"
50. .112
                                                                                                                                                                             Location/Qualifiers
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Percent Identity: 59.259
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US-09-142-524-1 x E11679
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                     TITLE
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                                    CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 792)
1 (bases 1 to 792)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster accessory gland protein Acp29AB (Acp29AB) \min_{n \in \mathbb{N}A_{+}} complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wolfner,M.F., Harada,H.A., Bertram,M.J., Stelick,T.J., Kraus,K.W., Kalb,J.M., Lung,Y.O., Neubaum,D.M., Park,M. and Tram,U. New genes for male accessory gland proteins in Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g2772590
                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (17-JAN-1997) Genetics and Development, Cornell
University, 423 Biotechnology Building, Ithaca, NY 14853-2703, USA
                                                                                                                                                                                                                                                                                                                                                                 Insect Biochem. Mol. Biol. 27 (1997) In press 2 (bases 1 to 792) Wolfner, M.F., Harada, H.A., Bertram, M.J., Stelick, T.J., Kraus, K.W., Kalb, J.M., Lung, Y.O., Neubaum, D.M., Park, M. and Tram, U.K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fruit fly.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.895
70.370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:32644"
/organism="unidentified"
                                                                                                                                                                                                              /organism="Drosophila melanogaster"
/strain="Canton S"
/db_xref="taxon:7227"
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29. .733
                                                                                           fluid"
                                                                                                                                  /tissue_type="accessory gland"
/sex="male"
/gene="Acp29AB"
/function="responsible for physiological and behavioral
                                                                                                                note="products of this tissue form part of the seminal
                                                                                                                                                                           /map="29AB"
                                                                                                                                                                                         /chromosome="2"
                                                                                                                                                                                                                                                                                       ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   113. .1174
/product="Cha o I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             792 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length: 27
Gaps: 0
Percent Identity: 59.259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-JAN-1998
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alignment_block:
US-09-142-524-1 x DMU85758
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: gb_ro:RRRPS18A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: DMU85758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VERSION
                                                                                                                                                                                                                           TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              390 ATTTTCACATCGAGAAGAATCTAATGCAAACTTGGTTTGAGGCATATGTC 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      290 CAGCTTCAGCCGTTAAAGATTATAATGCGACACCATGCATCCAACATCAA 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          490 GCTGGATGGCATCTTGGCGTTAGCACCCAACAATAGCTACTGG 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  440 ACATGTCGTAAAATGAACGGTCATCTGGCGAACATCCAGGATGAGAAGGA 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      340 AGCGTCTAACAACATCAAGATGAGACGATTCGAGAAAGTTGGCTCCAGAC 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 gValAspGlyIleIleAlaAlaTyrGlnAsnProAlaSerTrp 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53 SerLeuLysLeuThrSerGlyLysIleAlaSer.....ArgAr 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25 ......IleIleHisGlyArgArgIleAspIlePheAlaSerLysA 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 GlnPheGlyProAsnArgArgValPheIleLysArgValSerAsnVal..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      snPheHisLeuGlnLysAsnThrIleGlyThr.....GlyArgArgIle 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RRRPS18A 516 I
R.rattus ribosomal
X57529 S51078
                                                                                                                                                                                                                   Chan Y.L., Paz,V. and Wool,I.G.
The primary structure of rat ribosomal protein S18
Biochem. Biophys. Res. Commun. 178 (3), 1212-1218 (1991)
                                                                                                                                                                                                                                                                                                                               Submitted (06-FEB-1991) Y.L. Chan, 58th Street, Chcago IL 60637, U S A 2_ (bases 1 to 516)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

1. (bases 1 to 516)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g433446
x57529.1 GI:433446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chan, Y.L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       black rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ribosomal protein S18.
                                                                                                                                                                                               91337062
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="accessory gland protein Acp29AB"
/protein_id="AABB6382.1"
/protein_id="AABB6382.1"
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/db_xref="Gi:2772591"
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/translation="MYASNILYILA"
/translation="MYASNILYILA"
/translation="MYASNILYILA"
/translation="MYASNILYILA"
/translation="MYASNILYILA"
/translation="MYASNILYILA"
/translation="MYASNILYILA"
/translation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72.00
1.532
58.025
/strain="Sprague-Dawley"
/db_xref="taxon:10117"
                                                                               /organism="Rattus rattus"
                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             155 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       516 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from: 1 to: 792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps: 3
Percent Identity: 25.926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein S18 mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     162 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             193 t
                                                                                                                                                                                                                                                                                                                                                                                           SA
                                                                                                                                                                                                                                                                                                                                                                                                                               University of Chicago, 920 East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ROD
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FEATURES
                                                                                                                                                                                                                                                                         REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                     KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: gb_ro:MUSKE3B
                                                                                                                                                                                                                                                                                                                                                     SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
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                                                                                                                                                                           JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                              ERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: RRRPS18A from: 1 to: 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-142-524-1 x RRRPS18A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality: 70.00 Ratio: 1.707
Percent Similarity: 51.899
                                                                                                                                                                                                                                    TITLE
                                                                                                                                                                                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                                                                         AUTHORS
                      gene
                                                                               5'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           235 TGTGATCACCATCATGCAGAACCCACGACAATACAAG 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   185 ATTGACCTCACCAAGAGGGCTGGGGAGCTCACGGAGGACGAGGTGGAGCG 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            140 .....GGTGTGGGGGGGAGATACGCTCATGTGGTGTTGAGGAAAGCAGAC 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 yIleIleAlaAlaTyrGlnAsnProAlaSerTrpLys 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52 IleSerLeuLysLeuThrSerGlyLysIleAlaSerArgArgValAspGl 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45 hrileGlyThrGlyArgArg......51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28 yArgArgIleAspIlePheAlaSerLysAsnPheHisLeuGlnLysAsnT 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53 CCCGAGAAGTTTCAGCACATCCTGCGAGTACTCAACACCAACATCGATGG 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 ProAsnArgArgValPheIleLysArgValSerAsnValIleIleHisGl 28
                                                                                                                                                                                                                                                                                                                              ribosomal protein; ribosomal protein S13 homologue. Mus musculus cDNA to mRNA. Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                    g198579
м76763.1 GI:198579
                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus ribosomal protein (Ke-3) mRNA, complete cds
                                                                                                                                                                           92182530
                                                                                                                                                                                                                protein S13
                                                                                                                                                                                                                  The murine MHC encodes a mammalian homolog of bacterial ribosomal
                                                                                                                                                                                                                                                 MacMurray, A.J.
                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mamm
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                M76763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MUSKE3B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
                                                                                                                                                                                                                                               (bases 1 to 525)
Murray, A.J. and Shin, H.S.
                                                                                                                                                                                   Genome 2 (2), 87-95 (1992)
                    /note="putative"
23. .525
                                                                                                                                                     Location/Qualifiers
/gene="Ke-3"
                                                         /partial
                                                                                              /db_xref="taxon:10090"
                                                                                                            /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="SWISS-PROT:P25232"
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LDNKLREDLERLKKIRAHRGLRHFWGLRVRGQHTKTTGRRGRTVGVSKKK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="ribosomal protein S18"
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/db_xref="plb:9433447"
/db_xref="GI:433447"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="pMCS13-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        133 с
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 525 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length: 79
Gaps: 2
Percent Identity: 30.380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    159 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA
                                                                                                                                                                                                                                                                                                    Mammalia;
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REFERENCE
                                                                                                                                                                                                                                                                 ACCESSION
                                                                                                                                                                                                                                                                                                                  seq_name: gb_pl2:AF106662
                                                                                                                                                                                                           KEYWORDS
                                                                                                                                                                                                                               VERSION
                                                                                                                                                                                                                                                                                        DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: MUSKE3B from: 1 to: 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality: 70.00
Ratio: 1.707
Percent Similarity: 51.899
                           TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-142-524-1 x MUSKE3B
                                                                                                                                                                     ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 170 ATCGACCTCACCAAGAGGGCTGGAGAACTCACGGAGGATGAGGTGGAGCG 219
                                                                                                                                                                                                                                                                                                                                                                                                      220 AGTGATCACCATCATGCAGAACCCACGACAGTACAAG 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125 .....GGCGTGGGGCGAGATATGCTCATGTGGTGTTGAGGAAAGCAGAC 169
                                                                                                                                                                                                                                                                                                                                                                                                                                          68 yIleIleAlaAlaTyrGlnAsnProAlaSerTrpLys 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52 IleSerLeuLysLeuThrSerGlyLysIleAlaSerArgArgValAspGl 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45 hrlleGlyThrGlyArgArg......51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polyA_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28 yArgArgIleAspIlePheAlaSerLysAsnPheHisLeuGlnLysAsnT 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 ProAsnArgArgValPheIleLysArgValSerAsnValIleIleHisGl 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38 CCTGAGAAGTTCCAGCACATTTTGCGAGTACTCAACACCAACATCGATGG 87
                                                       Juniperus ashei
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukhryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Coniferopsida; Coniferales;
Cupressaceae; Juniperus.
1 (bases 1 to 1104)
allergen, Jun a 1
      Molecular cloning of mountain cedar (Juniperus ashei) pollen major
                                        Brooks, E.G.
                                                 Midoro-Horiuti, T.M., Goldblum, R.M., Kurosky, A., Wood, T.G. and
                                                                                                                                                                                  Ozark white cedar.
                                                                                                                                                                                                                        ĀF106662.1 GI:4138876
                                                                                                                                                                                                                                                                     Juniperus ashei pollen major allergen 1-1 mRNA, complete cds AF106662
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            502. .507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MSLVIPEKFQHILRVLNTNIDGRRKIAFAITAIKGVGRRYAHVV
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                                                                                                                                                                                                                                                                                                     1104 bp
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
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Midoro-Horiuti,T.M., Goldblum,R.M., Kurosky,A., Wood,T.G. and
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Juniperus ashei pollen major allergen 1-2 mRNA, complete cds.
AF106663
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                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Coniferopsida; Coniferales;
                                                                                                                                                                                                                                                                                                               Juniperus ashei
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Submitted (12-NOV-1998) Department of Pediatrics, Child Health
                     Brooks, E.G.
Direct Submission
                                                                    2 (bases 1 to 1104)
Midoro-Horiuti,T.M., Goldblum,R.M., Kurosky,A., Wood,T.G.
                                                                                                            Unpublished
                                                                                                                              Molecular cloning of mountain cedar (Juniperus ashei) pollen major allergen, Jun a 1
                                                                                                                                                                                                Midoro-Horiuti, T.M., Goldblum, R.M., Kurosky, A., Wood, T.G. and
                                                                                                                                                                                                                                               Cupressaceae; Juniperus.
                                                                                                                                                                                                                                                                                                                                         Ozark white cedar.
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3.842
70.370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="GI:4138877"
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                                                                                                           TITLE
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TITLE
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            CDS
                                                                    source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
                                                                                                                                                                                                  Direct Submission
Submitted (07-FEB-1997) to the DDBJ/EMBL/GenBank databases.
Noriyuki Hamasima, STAFF-Institute, Animal Genome Research Program
Team; 446-1 Ippaizuka, Kamiyokoba, Tsukuba, Lbaraki 305, Japan
(E-mail:hamasima@gene.staff.or.jp, Tel:0298-38-2190,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sus scrofa mRNA for
                                                                                                           Unpublished (1997
                                                                                                                            Kimura,M., Kawakami,K., Suzuki,H. and Hamasima,N. Cloning of the pig homolog of bacterial ribosomal protein S13
                                                                                                                                                                                                                                                                                                             Hamasima, N.
                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Artiodactyla; Suiformes; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                        Sus scrota
                                                                                                                                                                                                                                                                                                                                                                                                         Sus scrofa cDNA to mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                         ribosomal protein S13
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                                                                                                                                                                       (sites)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="maspellavlvelcaivscysdnpidscwrgdsnwdqnrmklad
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vmllghddtydddkskkvtvaknogenagormfrakgglvhyannnydpwniyaigg
ssnptilsegnsftapsesykkevtkrigcespsacanwvwrstrdafingayfvssg
kteetriynsneafkvengnaapqltknagvvt"
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3.842
70.370
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30. .488
                                                                                      Location/Qualifiers
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                                                                          . 528
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Gaps: 0
Percent Identity: 55.556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ribosomal protein, complete cds.
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BASE COUNT
ORIGIN
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US-09-142-524-1 x AB000911
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality: 70.00
Ratio: 1.707
Percent Similarity: 51.899
227 TGTAATCACCATTATGCAGAATCCTCGCCAATACAAG 263
                                                                       ||||:::|||
177 ATCGACCTCACCAAGAGGGCAGGAGGACGACGAGGATGAGGTGGAACG 226
                                                                                                                                                       45 hrileGlyThrGlyArgArg......51
||||:::|||||||
||132 .....GGTGTAGGACGGAGATATGCTCATGTGGTGTTGAGGAAAGCAGAC 176
                       68 yIleIleAlaAlaTyrGlnAsnProAlaSerTrpLys 80 :::|||::: |||
                                                                                                 52 IleSerLeuLysLeuThrSerGlyLysIleAlaSerArgArgValAspGl 68
                                                                                                                                                                                                                                       28 yArgArgIleAspIlePheAlaSerLysAsnPheHisLeuGlnLysAsnT 45
                                                                                                                                                                                                                                                                                                                           12 ProAsnArgArgValPheIleLysArgValSerAsnValIleIleHisGl 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   144 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="ribosomal protein"
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a 127 c 152 g 105 t
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Gaps: 2
Percent Identity: 30.380
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N\_Geneseq\_36:Q91972 N\_Geneseq\_36:T22169 N\_Geneseq\_36:V71744

48.00 51.00 55.50

122.51 122.28 122.22

31.85 32.80 33.06

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N_Geneseq_36:Q85341
N_Geneseq_36:Q95992
N_Geneseq_36:V28657
N_Geneseq_36:061403
                                                                                                                                                                                                                                                                 N_Geneseq_36:N30014
N_Geneseq_36:T61025
N_Geneseq_36:T67872
N_Geneseq_36:X13360
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N_Geneseq_36:735009
N_Geneseq_36:715873
N_Geneseq_36:711126
N_Geneseq_36:748588
N_Geneseq_36:748588
N_Geneseq_36:778596
N_Geneseq_36:778590
N_Geneseq_36:778591
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N_Geneseq_36:718102
N_Geneseq_36:738519
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                          N_Geneseq_36:x52269
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79 Enterococcus faecalis genome of
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71 Tomato fruit ripening specific
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Nucleotide sequence of the end
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Cytidine monophospho-N-acetyln
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seq_documentation_block:
ID 066050 standard; DNA;
AC 066050;
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DE Japanese cedar pollen
KW Cedar pollinosis; dia
OS Crytomeria japonica.
PN W09411512-A,
PN W0941512-A,
PD 26-MAY-1994.
PF 12-NOV-1992; US-97517
PA (IMMU-) IMMULOGIC PHA
PI Brauer A, Kuo M,
PD WPI; 94-183513/22, Po
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Ratio: 5.211
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W09411512-A.
26-MAY-1994.
12-NOV-1993; U11000.
12-NOV-1993; US-975179.
(1MUU-) INMULOGIC PHARM CORP.
Brauer A, Kuo M, Pollock J,
WPI; 94-183513/22.
                                                                                                                      Crytomeria japonica.
                                                                                                                               Japanese cedar pollen allergen Cry j II DNA fragment Cedar pollinosis; diagnostic; ss.
                                                                                                                                                                  01-FEB-1995 (first entry)
                                                                                                                                                                                                    Q66050 standard; DNA; 1395 BP.
                                                                                                                                                                                                                                                                                            594 AACAGGG 600
                                                                                                                                                                                                                                                                                                                                                      544 ATTGATATCTTTGCATCTAAAAACTTTCACTTACAAAAGAACACGATAGG 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Pages 26-27; 46pp; Japanese. 084044 encodes R69791 Japonicum allergen residues 55-514, from which the antiallergic peptides R69809 were derived. The peptides ability to inhibit the cross-linking of an allergen, to an IgE antibody can be used in the prevention and treatment of allergic diseases. Sequence 1380 BP; 456 A; 252 C; 316 G; 356 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; R69791.
Peptide antiallergic agent - inhibits cross-linking of allergen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-1994; J01164.
16-JUL-1993; JP-177008.
01-SEP-1993; JP-217725.
07-APR-1994; JP-069336.
                                                                                                                                                                                                                                                                                                                                                                         31 IleAspIlePheAlaSerLysAsnPheHisLeuGlnLysAsnThrIleGl 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Japonicum allergen (residues 55-514) encoding cDNA. Japonicum allergen; redidues 55-514; induced histamine release; antiallergic peptide; IgE cross-linking inhibition; ds.
                                                                                                                                                                                                                                                                                                                           47 YThrGly 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        with IgE antibody
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/note= "residues 55-514"
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! Human gene signature HUMGS03
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US-09-142-524-1 x Q66050
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US-09-142-524-1 x Q66049
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The sequence is of a Japanese cedar pollen allergen Cry j IIA fragment. The DNA and its fragments can be used for diagnosis treatment of Japanese cedar pollinosis and to identify similar sequences in other plants.

See also Q66048 67.

Sequence 1395 BP; 460 A; 257 C; 318 G; 360 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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12-NOV-1992; US-975179.
(IMMU-) IMMULOGIC PHARM CORP.
Brauer A, Kuo M, Pollock J, Yeung S;
WPI: 94-183513/22.
Allergenic Cry j II protein and fragments from Japanese cedar pollen - used to diagnose, treat and prevent Japanese cedar pollen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   606 AACAGGG 612
                                                                                                                                                                                                                                                                              The sequence is of a Japanese cedar pollen allergen Cry j IIA fragment. The DNA and its fragments can be used for diagnosis and treatment of Japanese cedar pollinosis and to identify similar sequences in other plants.

See also Q66048-67.

Sequence 1410 BP; 467 A; 258 C; 322 G; 363 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Japanese cedar pollen allergen Cry j II DNA fragment.
Cedar pollinosis; diagnostic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Crytomeria japonica.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q66049 standard; DNA; 1410 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31 IleAspIlePheAlaSerLysAsnPheHisLeuGlnLysAsnThrIleGl 47
                             571 ATTGATATCTTTGCATCTAAAAACTTTCACTTACAAAAGAACACGATAGG
                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 48; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47 yThrGly 49
                                                                                                                                                                                                                                                                                                                                                                                                   pollinosis
47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality: 99.00
Ratio: 5.211
Similarity: 100.000
                                                 yThrGly 49
                                                                                                                                                                                                                Quality:
                                                                                                                                                                                                 Ratio:
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5.211
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Gaps: 0
Percent Identity: 100.000
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Percent Identity: 100.000
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ISECTOR PROPERTY OF THE PROPER
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US-09-142-524-1 x Q66051
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   seq_documentation_block:
ID Q84045 standard; cD
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Ratio: 5.211
Percent Similarity: 100.000
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                                                            26-JAN-1995.

15-JUL-1994; J01164.

16-JUL-1993; JP-177008.

101-SEP-1993; JP-217725.

07-APR-1994; JP-059336.

(MEIP) MEIJI MILK PROD CO LTD.

Kino K, Kohno Y, Komiyama N, S

WPI; 95-067159/09.
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Disclosure; Page 50; 89pp; English.

The sequence is of a Japanese cedar pollen allergen Cry j IIA fragment. The DNA and its fragments can be used for diagnosis treatment of Japanese cedar pollinosis and to identify similar sequences in other plants.

See also Q66048-67.

Sequence 1479 BP; 490 A; 268 C; 337 G; 384 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-NOV-1993; U11000.
12-NOV-1992; US-975179.
(IMMU-) IMMULOGIC PHARM CORP.
Brauer A, Kuo M, Pollock J, Yeung S;
WPI; 94-183513/22.
Allergenic Cry J II protein and fragments from Japanese cedar pollen - used to diagnose, treat and prevent Japanese cedar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Crytomeria japonica.
WO9411512-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Japanese cedar pollen allergen Cry j II DNA fragment.
Cedar pollinosis; diagnostic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1995 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pollinosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-SEP-1995 (first entry)
Japonicum allergen cDNA.
Japonicum allergen; induced histamine release; antiallergic peptide;
Japonicum allergen; induced histamine release; antiallergic peptide;
IgE cross-linking inhibition; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               690 AACAGGG 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q84045;
                                                                                                                                                                                                                                                                                                                                        W09502412-A.
                                                                                                                                                                                                                                                                                                                                                                                                    mat_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31 IleAspIlePheAlaSerLysAsnPheHisLeuGlnLysAsnThrIleGl 47
Peptide antiallergic agent - inhibits cross-linking of allergen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47 yThrGly 49
                                      P-PSDB;
                                          R69792
                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                             Sone T;
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100.000
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seq_documentation_block:
ID 090156 standard; DNA;
AC 090156 policy
DT 01-NOV-1995 (first e DE 01-NOV-1995 policy
DE 01-NOV-1995 policy
KW Japanese cedar; policy
KW Japanese cedar; policy
KW Japanese cedar; policy
KW Japanese cedar; policy
KW Japanese policy
FT cds
FT 
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Percent Similarity: 100.000
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Ratio: 5.211
Percent Similarity: 100.000
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03-WOY-1994, 308117.
05-NOV-1993, JP-299151.
20-DEC-1993, JP-344596.
27-DEC-1993, JP-346814.
New Japanese cedar pollen allergen polypeptide - and DNA coding for it, useful for treatment and diagnosis of cedar pollen allergy Claim 6; Page 29; 41pp; English.

The gene encoding an allergen of Japanese cedar pollen was isolated by PCR amplification using primers based on portions of the allergen protein. The gene was used for recombinant allergen production in E. coli (vector plasmid pKK-223-3).

Sequence 1545 BP; 508 A; 283 C; 351 G; 403 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    with IgE antibody
Disclosure; Pages 27-28; 46pp; Japanese.
0840/45 encodes R69792 Japonicum allergen, from which the antiallergic peptides R69845-R69809 were derived. The peptides ability to inhibit the cross-linking of an allergen to an IgE antibody can be used in the prevention and treatment of allergic diseases.

The prevention and treatment of allergic diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cryptomeria japonica.
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Japanese cedar; pollen; allergen; al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1995 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q90156 standard; DNA; 1545 BP.
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Percent Identity: 100.000
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AC DE COS OS PR
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US-09-142-524-1 x Q66048
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WO9502412-A.
26-JMX-1995.
15-JUL-1994; J01164.
16-JUL-1993; JP-177008.
01-SEP-1993; JP-217725.
                                                                                                                                                                                               _documentation_block:
                                                                                                             Japonicum allergen cDNA and flanking sequences.
Japonicum allergen; induced histamine release; ant
Japonicum allergen; induced histamine release; ant
Japonicum allergen cDNA and flanking sequences;
                                                                                                                                                Q84046;
27-SEP-1995 (first entry)
                                                                                                                                                                                Q84046 standard; cDNA; 1733 BP
                                                                                                                                                                                                                                                                                          Japonicum sp.
                                                                                                                                                                                                                                                797 AACAGGG 803
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The sequence is that encoding a Japanese cedar pollen allergen Cry j
II. The DNA and its fragments can be used for diagnosis and
tractment of Japanese cedar pollinosis and to identify similar
sequences in other plants.

See also Q66049-67.
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Brauer A, Kuo M, Pollock J,
WPI; 94-183513/22.
                                                                                                                                                                                                                                                                        47 yThrGly 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Allergenic Cry j II protein and fragments from Japanese cedar pollen - used to diagnose, treat and prevent Japanese cedar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Japanese cedar pollen allergen Cry j II. Cedar pollinosis; diagnostic; ss.
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26-MAY-1994.
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12-NOV-1992; US-975179
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                                                                 /*tag=
                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                 100.000
                                                                                                                        antiallergic peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           465 T;
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alignment_block: US-09-142-524-1 \times Q84046
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seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: N_Geneseq_36:T18102
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Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 29; 46pp; Japanese. 984046 encodes R69792 Japonicum allergen, from which the antiallers opertides R69845-R69809 were derived. The peptides ability to inhibit the cross-linking of an allergen, to an IgE antibody can be used in the prevention and treatment of allergic diseases. Sequence 1733 BP; 593 A; 294 C; 380 G; 466 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide antiallergic agent - inhibits cross-linking of allergen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MEIP) MEIJI MILK PROD CO LTD. Kino K, Kohno Y, Komiyama N, WPI; 95-067159/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    with IgE antibody
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                                                                                                                                                                                                                                                                                                                                                                                                                 5'utr
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Japan cedar pollen cDNA encoding Cry j II allergen. Allergen; epitope; overlapping peptide; Cry j II; cedar pollen; Sugi pollinosis; diagnosis; treatment; ss.
       Jaran cedar pollen allergen Cry j II epitope - comprises at least part of specified 460 amino acid protein Claim 2: Page 13-14: 17pp; Japanese.
T18102 encodes a Japan cedar pollen Cry j II allergen which is useful in the diagnosis, prevention and treatment of Sugi pollinosis, the allergic reaction to Japan cedar pollen. Significant regions of the allergen were identified using overlapping peptides of the full epitope derived from a Cry j II antigen specific T cell line (see R97871-R97960). Amino acids 66-80 (R97884) and 186-200 (R978908) of the full mature 460 amino acid allergen are the most
                                                                                                                                                                         J-NWV-1993; JP-276773.
26-MAY 1994; JP-134868.
(MEIP) MEIJI MILK PROD CO LTD.
WPI; 96-166249/17.
                                                                                                                                                                                                                                                                                               3/11/5
                                                                                                                                                                                                                                                                                                                          mat_peptide
                                                                                                                                                                                                                                                                                                                                                        signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                             Cryptomeria japonica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T18102 standard; cDNA to mRNA; 1733 BP
                                                                                                                                                                                                                                      07-NOV-1994;
                                                                                                                                                                                                                                                                    J08047392-A
                                                                                                                                                            P-PSDB; R93599
                                                                                                                                                                                                                                                   20-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47 yThrGly 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .6-AUG-1996 (first entry)
allergenic of the 90 peptides tested.
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                                                                                                                                                                                                                                        297840
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45. .206
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207. .:
                                                                                                                                                                                                                                                                                                  /*tag=
1590.
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                                                                                                                                                                                                                                                                                                                                                                                        .1589
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.1733
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                                                                                                                                                                                                                                                                                                                                               a
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Percent Identity: 100.000
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US-09-142-524-1 x T18102
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                                                                                                                                                                                                                                                   seq_documentation_block:
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                                                                                                                   alignment_block:
US-09-142-524-1 x T38518
                                                                                                                                                             Percent Similarity:
                                                                                     Align seg 1/1 to: T38518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chamaecyparis obtusa polien allergen Cha o I cDNA (B). Pollen allergen; Cha o I; T-cell epitope; prevention; treatment;
                                                                                                                                                                                                                                                                           The present sequence encodes the C. obtusa pollen allergen Cha of the T-cell epitopes of which can be used in the development of a preventive and treating agent for C. obtusa pollen pollinosis. C. obtusa pollen (2.4 kg) was degreased with diethyl ether, and dried at room temp. overnight. Cha o I was sepd. from it and purified. RNA was extracted from C. obtusa pollen, and mRNA and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J08176192-A.
09-JUL-1996.
21-DEC-1994; 335089.
21-DEC-1994; JP-335089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chamaecyparis obtusa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pollinosis; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T38518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31 IleAspIlePheAlaSerLysAsnPheHisLeuGlnLysAsnThrIleGl 47
                                                                                                                                                                                                                                                                dried at room temp.
purified. RNA was ex
cDNA derived.
                                                                                                                                                                                                                                                                                                                                                                  treating agent for C. obtusa pollen pollinosis Claim 10; Page 13; 17pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding chamaecyparis obtusa pollen allergen - T cell epitope(s) of which are useful in development of preventative and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; W04345
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                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                            (MEIP ) MEIJI MILK PROD CO LTD WPI; 96-368225/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38518 standard;
                             700 ATGAAGGTGACAGTGGCATTCAATCAATTTGGACCTAATGCTGGACAACG 749
17 eIleLysArgValSerAsnValIleIleHis
                                                        1 MetLysValThrValAlaPheAsnGlnPheGlyProAsnArgArgValPh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
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                                                                                                                                                                             Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1733 BP;
                                                                                                                                                                                                                                                     1125 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.211
100.000
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/note= "STOP codon absent"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               location/Qualifiers
                                                                                                                                                               74.00
3.895
70.370
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                                                                                          from: 1
                                                                                                                                                                                                                                                      327 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Identity:
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                                                                                                                                                                 Percent Identity: 59.259
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                                                                                         to: 1125
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                                                                                                                                                                                                                                                        211 C;
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                                                                                                                                                                                                                                                        264 G;
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750 AATGCCAAGGGCACGATATGGACTTATACAT

780

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seq_documentation_block:
ID 055272 standard; cDNA; 1170 BP.
AC 055272
DT 13-JUL-1994 (first entry)
DE Jun s I gene.
KW Japanese cedar; pollen allergen;
KW Japanese cedar; pollen allergen;
CS Juniperus sabinoides.
FH Key Location/Qualifie
FT cds 26. 1129
FT signal_peptide 26. 1129
FT mat_peptide 26. 1129
FT mat_peptide 89. 1129
FT w09401560-A. /*tag= c
                                                                                                                                                                                                                                                                               seq_name: N_Geneseq_36:Q55272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: T38519 from: 1 to: 1260
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                                                                                                                                                                                                                                                                                                                                                                          DNA encoding chamaecyparis obtusa pollen allergen - T cell pritope(s) of which are useful in development of preventative and treating agent for C. obtusa pollen pollinosis Claim 4: Pages 13-14; 17pp; Japanese.

The present sequence encodes the C. obtusa pollen allergen Cha o I the T-cell epitopes of which can be used in the development of a preventive and treating agent for C. obtusa pollen pollinosis. C. obtusa pollen (2.4 kg) was degreased with diethyl ether, and dried at room temp. overnight. Cha o I was sepd. from it and purified. RNA was extracted from C. obtusa pollen, and mRNA and
                                                                                                                                                                                                                                                                                                               799 AATGCCAAGGGCACGATATGGACTTATACAT
                                                                                                                                                   Japanese cedar; pollen allergen; allergy; treatment;
T cell epitope; sensitivity; detection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             _documentation_block;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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21-DEC-1994; JP-335089.
(MEIP) MEIJI MILK PROD CO LTD.
WPI; 96-368225/37.
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09-JUL-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-NOV-1996 (first entry)
Chamaecyparis obtusa pollen allergen Cha o I cDNA (A).
Pollen allergen; Cha o I; T-cell epitope; prevention; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; W04344.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pollinosis; ds.
Chamaecyparis obtusa.
                                                                                                                                                                                                                                                                                                                                             17 eIleLysArgValSerAsnValIleIleHis 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T38519;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1260 BP;
                                                                                                                                               sensitivity; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74.00
3.895
70.370
                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= a
/note= "sequence comprising nucleotides 113. .1174
is claimed, i.e. CDS minus STOP codon"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA; 1260 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   375 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Identity: 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   233 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  282 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                370 T;
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The process of which are useful in development of preventative and treating agent for c. obtusa pollen pollinosis claim 16; Page 16; 17pp; Japanese.

The present sequence encodes the C. obtusa pollen allergen Chao II, the T-cell epitopes of which can be used in the development of a preventive and treating agent for C. obtusa pollen pollinosis. C. obtusa pollen (2.4 kg) was degreased with C. dain the transport of a preventive and treating agent for C. obtusa pollen pollinosis. C. obtusa pollen (2.4 kg) was degreased with C. diethyl ether, and dried at room temp. overnight. Cha o II was sept. from it and purified. RNA was extracted from C. obtusa pollen, and mRNA and cDNA derived.

Sequence 1772 BP; 581 A; 328 C; 388 G; 475 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: N_Geneseq_36:T38521
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                                                                                                                                                                                                                                                  09-JUL-1996.
21-DEC-1994; 335089.
21-DEC-1994; JP-335089.
(MEIP ) MEIJI MILK PROD CO LTD.
WEI; 96-368225/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chamaecyparis obtusa polien allergen Cha o II cDNA.
Pollen allergen; Cha o II; T-cell epitope; prevention; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        725 ATGAAAGTGACAGTGGCGTTCAATCAATTTGGACCTAATGCTGGGCAAAG 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chamaecyparis obtusa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-NOV-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     775 AATGCCAAGGGCACGATATGGACTTGTACAT 805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 16; 137pp; English.

The sequence is that encoding Jun's I, a homologue of the Japanese cedar pollen allergen Cry J I. Antigenic peptides derived from it can be used for the treatment and diagnosis of allergies associated with Japanese cedar pollen.

With Japanese cedar pollen.

Sequence 1170 BP; 350 A; 215 C; 268 G; 337 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T38521 standard; cDNA; 1772 BP.
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Bond JF, Garman RD, Griffith IJ, Kuo M, Pollock J;
WPI; 94-035065/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-JAN-1994.
15-JAN-1993; U00139.
10-JUL-1992; WO-U05661.
01-SEP-1992; US-938990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antigens derived from Japanese cedar pollen allergen Cry j I contain at least two T cell epitope(s), used to treat or diagnose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 eIleLysArgValSerAsnValIleIleHis 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; R45577.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MetLysValThrValAlaPheAsnGlnPheGlyProAsnArgArgValPh 17
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                                                                                                                                                                                                                                                                                                                                                /*tag= a
/note= "sequence comprising nucleotides
is claimed, i.e. CDS minus STOP codon"
                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers 32. .1576
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3.842
70.370
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Gaps: 0
Percent Identity: 55.556
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alignment_block:
US-09-142-524-1 x T38521
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ID Q71601 standard; cDNA to mRNA; 1317 BP.
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                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                alignment_scores:
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                                                                                                                                                                     alignment_block:
                                                                                                                        Align seg 1/1 to: Q71601
                                                                                                                                                      US-09-142-524-1 x Q71601
                                                                                                                                                                                                    Percent Similarity:
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07-MAR-1995 (first entry)
Transse cedar pollen antigen CryjI cDNA.
Transse cedar; pollen antigen; allergen; CryjI; sugi; pollinosis;
                                                                                                                                                                                                                                                                                          Sugi (Japanese cedar) pollen antigen CryjI - is useful for diagnosis, treatment and prevention of sugi pollinosis claim 6; Page 5-7; 9pp; Japanese cedar ("sugi") pollen allergen The coding sequence for the Japanese cedar ("sugi") pollen allergen CryjI was isolated from a cDNA library prepared from polyA mRNA. All or part of the CryjI protein can be used for diagnosis, treatment and prevention of sugi pollinosis.

sequence 1317 BP; 410 A; 230 C; 284 G; 393 T;
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07-JAN-1993; JD-001116.
07-JAN-1993; JD-001116.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cryptomeria japonica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                    (MEIJ) MEIJI SEIKA KAISHA.
WPI; 94-268680/33.
P-PSDB; R60166.
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811 AATGCCCAGGGCACGATATGGACTTGTACAT 841
                                                            761 ATGAAGGTGACAGTGGCGTTCAATCAATTTGGACCTAACTGTGGACAAAG 810
                             17 eIleLysArgValSerAsnValIleIleHis 27
                                                                                          1 MetLysValThrValAlaPheAsnGlnPheGlyProAsnArgArgValPh 17
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/*tag= c

.184. .1317
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62. .124
/*tag= b
125. .1183
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94.737
                                                                                                                                                                                                    71.00
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                                                                                                                            from: 1 to: 1317
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                                                                                                                                                                                                     Percent Identity: 55.556
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                                                                                                                                                                                                                                      Length:
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seq\_name: N\_Geneseq\_36:Q35304

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seq_documentation_block:
ID 035304 standard; cDNA to mRNA; 1337 BP.
AC 035304,
DE 03-JUN-1993 (first entry)
DE Cry J I gene.
KW Japanese cedar pollen; allergen; antigen;
OS Cryptomeria Japonica.
Cryptomeria Japonica.
Cryptomeria Japonica.
Cryptomeria Japonica.
FT cds 66. .118
FT signal_peptide 66. .118
FT signal_peptide 129. .1187
FT ww09301213-A.
PR 12-JUL-1993 US-729134.
PR 12-JUL-1991; US-730452.
PR 12-JUL-1993; US-730452.
PR 12-JUL-199; US-730452.
PR 12-JUL-1993; US-730452.
PR 12-JUL-1993; US-73045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PT Nucleic acid sequence encoding Cryptomeria japonica allergen provided reactment and prevention of allergic reactions provided for the diagnosis treatment and prevention of allergic reactions provided for the diagnosis treatment and prevention of allergic reactions provided for the diagnosis treatment and prevention of allergic reactions. Provided for the diagnosis code constant tree. RNA was prepared and used constant paper and the contain a partial constant provided and 193 bp clone, UC71.6, found to contain a partial constant provided for the synthesise code. The code was subjected to successive rounds of the sequence of Cry j. A secondary prox was performed and clones for consequence of Cry j. I or an antigent fragment of it may be used consequence coder pollen allergen. It is capable of modifying both the contains allergen. The sequence to Cry j. I and T. call response to a Cry j. I and T. call response to a Cry j. I and T. call response to a Cry j. I and T. call response to a Cry j. I and T. call response to a Cry j. I and T. call response to a Cry j. I and T. call response to a Cry j. I and T. call response to a Cry j. I and T. call response to a Cry j. I and T. call response to a Cry j. I and T. call response to a Cry j. I and T. call response to a Cry j. I and T. call response to a Cry j. I and T. call response to a Cry j. I and T. call response to a Cry j. I and T. call response to a Cry j. I and T. call response to a Cry j. I and T. call response to a Cry j. I and T. call response to a Cry j. I and T. call response to a Cry j. I and T. call response to a Cry j. I and T. call response to a Cry j. I and T. call response to a Cry j. I and T. call response to a Cry j. I and T. call response to a Cry j. I and T. call response to a Cry j. I and T. call response to a Cry j. I and T. call response to a Cry j. I and T. call response to a Cry j. I and T. call response to a Cry j. I and T. call response to a Cry j. I and T. call response to a Cry j. I and T. call response to a Cry j. I and T. call response to
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US-09-142-524-1 x Q35304
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                                                                                                                                                                                                    765 ATGAAGGTGACAGTGGCGTTCAATCAATTTGGACCTAACTGTGGACAAAG 814
815 AATGCCCAGGGCACGATATGGACTTGTACAT 845
                                                                                         17 eIleLysArgValSerAsnValIleIleHis 27
                                                                                                                                                                                                                                                                                                         1 MetLysValThrValAlaPheAsnGlnPheGlyProAsnArgArgValPh 17
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gb_est31:F26562
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gb_est12:AA300816
gb_est20:AA815996
gb_est20:AA816017
                                                      gb_est14:AA381322
gb_est13:AA379368
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gb_est5:H95871
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                                                                                                                                                                                                                                                                   gb_est13:AA356932
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gb_est13:AA379470
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gb_est13:AA379609
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Query length: 80
Database: EST:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database sequences: 2546578
Database length: 986266752
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0.0300
0.0818
AA659604 ntt33e10.sl NCI_CGAP_Pr
AA498109 v175h08.rl Stratagene
AA198180 mv48e09.rl Soares mous
AA248242 csg1717.seq.F Human fe
AA036117 AU036117 Polyandrocarp
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AU036104 AU036114 Polyandrocarp
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AA603354 np06a11.sl NCI_CGAP_PL
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AA31359 EST94431 ACTLVated T-C
AA379609 EST92467 Skin tumor I
AA288347 mr52c03.rl Life Tech m
AA378031 EST90680 Synovial sarc
AA313411 ai61e03.sl Soares_test
AA379470 EST92568 Skin tumor I
AA379470 EST92568 Skin tumor I
AA349283 EST55908 Infant adrena
D55079 HUM1648030 Clontech huma
AA381326 EST94471 Activated T-C
AA381326 EST94471 Activated T-C
AA381326 EST94676 Activated T-C
D53913 HUM1238080 Clontech huma
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AA3792506 vs92b06.rl Barstead mc
AA815096 vr14b09.rl Barstead mc
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AA815096 vs92b06.rl Barstead mc
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AA390464 EST34615 Embryo, 6 wee
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AA330464 EST34615 Embryo, 9 wee
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AA319368 EST92188 Skin tumor I
AA350159 EST6279 Lymph node I
AA353178 EST61276 Activated T-C
AA351178 EST61276 Activated T-C
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                                        alignment_block:
                                                                                                            alignment_scores:
    Quality:
                                                                                                                                                                                          ORIGIN
                                                                                                                                                                                                             BASE COUNT
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AUTHORS
TITLE
                  US-09-142-524-1 x AA659604
                                                                          Percent Similarity:
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gb_est13:AA379646
gb_est14:AA381374
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LOCUS AA659604
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 377.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 519)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Tumor Gene Index
Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      On May 9, 1995 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                 histologically-determined to be fully malignant prostate cancer cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of PCR applied to the cDNA with an adaptor specific primer, and the resulting PCR product subcloned into pAMP10 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not David Krizman. This library was constructed by a 114 c 143 g 117 t
        80.00
2.000
54.054
                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="45 years old"
/lab_host="PH10B"
/lab_host="PH10B"
/note="Vector: pAmP10; Site_1: Not1; Site_2: EcoRI; 1st
Strand cDNA was primed with oligo(dT)17 on 50 ng of
DNAse-treated, total cellular RNA obtained from
5,000-10,000 microdissected cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="NCI_CGAP_Pr3"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="IMAGE:1203210"
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Length: 74
Gaps: 2
Percent Identity: 32.432
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AA379646 EST92511 Skin tumo
AA381374 EST94447 Activated
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Skin tumor
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        228 GCAGAATCCACGCCAGTACAAG 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46 TATATTTTGCGAGTACTCAACATTATCATCGATGGGCGGCGGAAAATAGC 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73 rGlnAsnProAlaSerTrpLys 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57 ThrSerGlyLysIleAlaSerArgArgValAspGlyIleIleAlaAlaTy 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 v175h08.rl Stratagene mouse testis (#937308) Mus musculus cDNA clone IMAGE:918111 5' similar to gb:M76763 Mus musculus ribosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein (MOUSE);, mRNA sequence.
AA498109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Waterston,R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         I (bases 1 to 513)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Geisel, S., Kucaba, T., Lacy, M., Tan, F., Underwood, K., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA498109
                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ĀA498109.1 GI:2233132
                                                                                                                                                                                                                                                                                                                                                                                                                        MGI:530327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  house mouse.
                                                                                                                                                                                                                                                                                                                                                                         vector to vector
                                                                                                                                                                                                                                                                                                                                                                                                  Putative full length read
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to: AA659604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sep 12, 1996 this sequence version replaced g1:1288654
                                                                                                                                                                                                                                                                                                          cor to vector length is 514 primer: -28ml3 rev1 ET from Amersham h quality sequence stop: 441.
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/tissue_type="10-12 week old"
/dev_stage="10-12 week old"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: testis; Vector: pBluescript SK-; Site_1:
                                                                                                                                 /strain="Inbred CD-1"
/db_xref="taxon:10090"
/clone="MAGE:918111"
/clone_1ib="Stratagene mouse testis (#937308)"
                                                                                                      /sex="males"
                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                       organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus.
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alignment_block:
US-09-142-524-1 x AA498109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: gb_est11:AA198386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOURCE
ORGANISM
                                                                                                                                                                                                                                                                           COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ERSION
                                                                                                                                                                                                                                                                                                   JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 .....GGCGTGGGGCGGAGATATGCTCATGTGGTGTTGAGGAAAGCAGAC 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    216 AGTGATCACCATCATGCAGAACCCACGACAGTACAAG 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   166 ATCGACCTCACCAAGAGGGCTGGAGAACTCACGGAGGACGAGGTGGAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28 yArgArgIleAspIlePheAlaSerLysAsnPheHisLeuGlnLysAsnT 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34 CCTGAGAAGTTCCAGCACATTTTGCGAGTACTCAACACCATCATCGATGG 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 ProAsnArgArgValPheIleLysArgValSerAsnValIleIleHisGl 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52 IleSerLeuLysLeuThrSerGlyLysIleAlaSerArgArgValAspGl 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45 hrlleGlyThrGlyArgArg.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 yIleIleAlaAlaTyrGlnAsnProAlaSerTrpLys 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA198386 520 bp mRNA EST 22-JAN-1997 mv48e09.rl Soares mouse 3NME12 5 Mus musculus cDNA clone IMAGE:658312 5' similar to gb:M76763 Mus musculus ribosomal protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 520)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuqu Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

Waterston, R.

Waterston, R.

Waterston, R.

When Machu-Hill Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MOUSE);, mRNA sequence.
AA198386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:404160
                                                                                           Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                          WashU-HHMI Mouse EST Project Washington University School of MedicineP
                                                                                                                                                                                                                                                                         On Sep 12, 1996 this sequence version replaced gi:1394766.
                                                                                                                                                                                                                                                                                                      Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA198386.1 GI:1794063
                                                                                                                                                   4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                            Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio:
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1.833
53.165
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Gaps: 2
Percent Identity: 31.646
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dietrich, N., Dubuque, T.,
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seq_name: gb_est11:AA248242
                                                  KEYWORDS
                                                                          VERSION
                                                                                                                                                                                                                        seq_documentation_block:
                                                                                                                             ACCESSION
                                                                                                                                                                             DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: AA198386 from: 1 to: 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-142-524-1 x AA198386
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     ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                          242 CACGACAGTACAAG 255
                                                                                                                                                                                                                                                                                                                                                                                                                  192 AGAACTCACGGAGGATGAGGTGGAGCGAGTGATCACCATCATGCAGAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     142 GCTCATGTGGTGTTGAGGAAAGCAGACATCGACCTCACCAAGAGGGCTGG 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 YLYSILeAlaSerArgArgValAspGlyIleIleAlaAlaTyrGlnAsnP 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52 .....IleSerLeuLysLeuThrSerGl 59
                                                                                                                                                                                                                                                                                                                                                                          76 roAlaSerTrpLys 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36 erLysAsnPheHisLeuGlnLysAsnThrIleGlyThrGlyArgArg... 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 GCGAGTACTCAACACCAACATCGATGGGCGGCGGAAAATAGCCTTCGCCA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19 sArgValSerAsnValIleIleHisGlyArgArgIleAspIlePheAlaS 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 GTGACCGCCGCCATGTCTCTAGTGATCCCTGAGAAGTTCCAGCACATTTT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 ValThrValAlaPheAsnGlnPheGlyProAsnArgArgValPheIleLy 19
                                                                                                                                          AA248242 360 bp mRNA EST 11-MAR-1997 CSg1717.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens CDNA 5', mRNA sequence.
Homo sapiens
                                                  EST
                                                                        AA248242.1 GI:1878895
                                                                                                                             AA248242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        with a modified polylinker; Site_1: Not I; Site_2: Eco RI; ist strand cDNA was primed with a Not I: Oligo(dT) primer ist strand cDNA was primed with a Not I: Oligo(dT) primer ist strand cDNA was primed with a Not I: Oligo(dT) primer ist strand cDNA was primed with a Not I: Oligo(dT) primer ist state univ.i; double-stranded by Minoru Ko, Wayne State Univ.i; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      quality sequence stop: 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.638
53.409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="fetus"
/dev_stage="12.5dpc total fetus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:10090"
/clone="IMAGE:658312"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Soares mouse 3NME12 5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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Gaps:
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ACCESSION
                                                 DEFINITION
                                                                                          seq_documentation_block:
                                                                                                                                           seq_name: gb_est29:AU036117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
US-09-142-524-1 x AA248242
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
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JOURNAL
                                                                                                                                                                                                                                                                            166 ATTGACCTCACCAAGAGGGCGGGAGAACTCACTGAGGATGAGGTGGACCG 215
                                                                                                                                                                                                                                                                                                                                                                         121 .....GGTGTGGGCCGAAGATATGCTCATGTGGTGTTGAGGAAAGCAGAC 165
                                                                                                                                                                                  216 TGTGATCACCATTATGCAGAATCCACGCCAGTACAAG 252
                                                                                                                                                                                                                           68 yIleIleAlaAlaTyrGlnAsnProAlaSerTrpLys 80
                                                                                                                                                                                                                                                                                                                           52 IleSerLeuLysLeuThrSerGlyLysIleAlaSerArgArgValAspGl 68
                                                                                                                                                                                                                                                                                                                                                                                                                     45 hrileGlyThrGlyArgArg......51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 GCGGCGGAAAATAGCCTTTGCCATCACTGCCATTAAG...... 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28 yArgArgIleAspIlePheAlaSerLysAsnPheHisLeuGlnLysAsnT 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 CCTGAAAAGTTCCAGCATATTTTGCGAGTACTCAACACCCAACATCGATGG 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 ProAsnArgArgValPheIleLysArgValSerAsnValIleIleHisGl 28
     AU036117 Polyandrocarpa misakiensis white spot budding stage Polyandrocarpa misakiensis cDNA, mRNA sequence.
AU036117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: 5' GAAATTAACCCTCACTAAAGGG 3'.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNAs from human fetal heart (1997)
Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1402306.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FORWARD: 5' GCCAAGCTCGAAATTAACCCTCACTAAAGGG
BACKWARD: 5' CCAGTGAATTGTAATACGACTCACTATAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Banting Institute, 100 College St., Toronto, Ontario, M5G1L5 Tel: 4169788758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Department of Laboratory Medicine and Pathobiology University of Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCR PRimers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Liew CC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 360)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11ewcc@utcc.utoronto.ca
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1.805
51.899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /Clone_lib="Human fetal heart, Lambda ZAP Express"
/lab_host="E. coli XL1-Blue"
/note="Vector: Lambda ZAP Express; Site_1: EcoRI; Site_2:
Xhol; mRNA was purified from human fetal hearts (8-10
weeks). cDNA was synthesized using a XhoI-oligo dT
adaptor-primer. EcoRI adaptors were ligated, followed by
predigested lambda ZAP Express."

84 c 100 g 74 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/map="907F10"
                                                              371 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCAGTGAATTGTAATACGACTCACTATAGGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Identity: 31.646
                                                                mRNA
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SOURCE
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US-09-142-524-1 x AU036117
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ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
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                                            seq_documentation_block:
LOCUS AA738025
                                                                                                        seq_name: gb_est19:AA738025
                       DEFINITION
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                                                                                                                                                                                                                                                                                                                                    191 ATCTGCTTGAAGGCCGATGTTGATCTCAGGAAACGTGCCCGGAGAACTGAC 240
                                                                                                                                                                                                                                                                                                                                                                                                                     149 .....ATGACTGCAGTCAAGGGAGTTGGAAGAAGATTCAGCAACTTG 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 AGAGGATGAAATCGACAGAGTTGTCACGATCATGCAGAATCCTCGCCAGT
                                                                                                                                                       291 ACAAG 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                             39 heHisLeuGlnLysAsnThrIleGlyThrGlyArgArgIleSer..... 53
                                                                                                                                                                                                                                                                                     62 aSerArgArgValAspGlyIleIleAlaAlaTyrGlnAsnProAlaSerT 79
                                                                                                                                                                                                                                                                                                                                                                              54 .....LeuLysLeuThrSerGlyLysIleAl 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 rAsnValIleIleHisGlyArgArgIleAspIlePheAlaSerLysAsnP 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83 AGTTTCAACACATTC...........TTTCGTATCAC 108
                                                                                                                                                                                                   79 rpLys 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 AlaPheAsnGlnPheGlyProAsnArgArgValPheIleLysArgValSe 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kawamura,K., Hayata,D., Fujiwara,S. and Yubisui,T. Serine protease inhibitors expressed in the process of budding of tunicates as revealed by EST analysis
J. Biochem. (1998) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stolidobranchia; Styelidae; Polyandrocarpa. 1 (bases 1 to 371)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polyandrocarpa misakiensis.
Polyandrocarpa misakiensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g4527078
AU036117.1 GI:4527078
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Tel: +81-888-44-8313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kochi University
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         On Jun 5, 1998 this sequence version replaced gi:3188168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
nx15d09.sl NCI_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1256177 similar to gb:x69150 408 RIBOSOMAL PROTEIN S18 (HUMAN);, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="polyandrocarpa misakiensis"
/strain="white spot"
/db_xref="taxxx:7723"
/clone_lib="Polyandrocarpa misakiensis white spot budding stage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.644
52.941
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83 c 100 g 84 t
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                                              520 bp
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Percent Identity: 25.882
                                              mRNA
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REFERENCE
AUTHORS
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality: 75.00
Ratio: 1.829
Percent Similarity: 51.899
                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to reverse of: AA738025 from: 1 to: 520
                                                                                                                                                                                                                                                                                                                                                                     US-09-142-524-1 x AA738025/rev
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                                                                                                           435 TCGGCGGAAAATAGCCTTTGCCATCACTGCCATTAAG...
                                                                                                                                                                                                              485 CCCGAAAGGTCCCAGCATATTCTGCGAGTACTCAACACCCAACATCGATGG 436
398 .....GGTGTGGGCCGAAGATATGCTCATGTGGTGTTGAGGAAAGCAGAC 354
                                                                                                                                                                                                                                                          12 ProAsnArgArgValPheIleLysArgValSerAsnValIleIleHisGl 28
                                                       45 hrIleGlyThrGlyArgArg.....
                                                                                                                                                       28 yArgArgIleAspIlePheAlaSerLysAsnPheHisLeuGlnLysAsnT 45
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AA738025
q2768782
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCI CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 402.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumor Gene Index
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                www-bio.lln1.gov/bbrp/image/image.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="pooled germ cell tumors"
/lab_host="DHIDB"
/lab_host="DHIDB"
/note="vector: pT7T3D-Pac (Pharmacia) with a modified
/note="vector: pt7T3D-Pac (Pharmacia) with a Not I
polylinker; lst strand cDNA was prepared from 3 pooled
perm cell tumors, and was then primed with a Not I
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT7T3
vector. Library is not normalized. Library was
constructed by Bento Soares and M. Fatima Bonaldo. "
07 a 145 c 125 g 141 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="IMAGE:1256177"
/clone_lib="NCI_CGAP_GC3"
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/db_xref="taxon:9606"
/map="20q13.2-q13.3"
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Gaps: 2
Percent Identity: 31.646
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alignment_scores:
Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: gb_est29:AU036104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
TITLE
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200 GTTGATCTCAGGAAACGTGCCGGAGAACTGACAGAGGATGAAATCGACAG 249
                                                                             150 TCAAGGGAGTTGGAAGAAGATTCAGCAACTTGATCTGCAAGAAGGCCGAT 199
                                                                                                                                                          118 ACGTAGAAAGATCGTCTACGCC.....ATGACTGCAG 149
                                      54 .....LeuLysLeuThrSerGlyLysIleAlaSerArgArgValAspG1 68
                                                                                                                        45 hrIleGlyThrGlyArgArgIleSer.....
                                                                                                                                                                                                23 YhrghrgIleAspIlePheAlaSerLysAsnPheHisLeuGlnLysAsnT 45
                                                                                                                                                                                                                                           68 CCAGAGAAGTTTCAACACATTCTTCGTATCACGAACACGAATATCGATGG 117
                                                                                                                                                                                                                                                                                  ProAsnArgArgValPheIleLysArgValSerAsnValIleIleHisGl 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               353 ATTGACCTCACCAAGAGGGCGGGAGAACTCACTGAGGATGAGGTGGAACG 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 yllelleAlaAlaTyrGlnAsnProAlaSerTrpLys 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52 IleSerLeuLysLeuThrSerGlyLysIleAlaSerArgArgValAspGl 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2-5-1, Akebono-cho, Kochi 780, Japan
Tel: +81-888-44-8313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         On Jun 5, 1998 this sequence version replaced gi:3188155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kawamura,K., Hayata,D., Fujiwara,S. and Yubisui,T. Serine protease inhibitors expressed in the process of budding tunicates as revealed by EST analysis
J. Biochem. (1998) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AU036104 Polyandrocarpa misakiensis white spot budding stage Polyandrocarpa misakiensis cDNA, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Kawamura K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stolidobranchia; St
1 (bases 1 to 320)
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Polyandrocarpa misakiensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fax: +81-888-44-8313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 kazuk@cc.kochi-u.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                      1.659
56.410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev_stage="budding stage"
70 c 85 g 68 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Polyandrocarpa misakiensis white spot budding stage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Polyandrocarpa misakiensis"
/strain="white spot"
/db_xref="taxon:7723"
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                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 78
Gaps: 2
Percent Identity: 25.641
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                                                                                                                          53
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                                                                      alignment_scores:
          Percent Similarity:
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ORIGIN
                   BASE COUNT
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68 yIleIleAlaAlaTyrGlnAsnProAlaSerTrp 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RS Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man.Wai, C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.Jr.,
Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, J.F., Li, Y.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,
Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
Initial assessment of human gene diversity and expression patterns
Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96026280
On Sep 12
                                                                                                                                                                                                                                                                                                                                                    For clone availability, additional sequence and exinformation related to this \mathtt{EST}, please check the
                                                                                                                                                                                                                                                                                                             Seq primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
                                                                                                                                                                                                                                                                                                                           Index (http://www.tigr.org/tdb/hgi/hgi.html)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                      Email: arkerlav@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 265)
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AA300566.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sep 12,
                   70
           /dev_stage="adult"
/note="Organ: testis; Vector: pBluescript SK-; Site_1:
ECORI; Site_2: XhoI"
61 c 68 g 62 t 4 others
                                                                                                                                                                 /db_xref="ATCC (inhost):192428"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                       /sex="male"
                                                                                                                                           /clone_lib="Testis tumor"
                                                                                                                                                                                                                          /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1996 this sequence version replaced gi:1395394.
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                                                                                                                                                                                                                                                                                                                                                    additional sequence and expression this EST, please check the TIGR Human
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Quality:

Ratio:

72.00 1.756 51.899

Percent Identity: 30.380

Length:

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alignment_block:
US-09-142-524-1 x AA300566
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LOCUS D76822
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KEYWORDS
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                                                                                                                                                                                     alignment_scores:
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                                                alignment_block:
US-09-142-524-1 x D76822
Align seg 1/1 to: D76822
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           212 TGTGATCACCATTATNCAGAATCCACGCCAGTACAAG 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  162 ATTGACCTCACCAAGAGGGCGGGGAGAACTCACTGAGGNTGAGGTGGAACG 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 ProAsnArgArgValPheIleLysArgValSerAsnValIleIleHisGl 28
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                                                                                                                                                                                                                                                                                                                                                                                               source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28 yArgArgIleAspIlePheAlaSerLysAsnPheHisLeuGlnLysAsnT 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MUS78A01 mouse embryonal carcinoma cell line F9 Mus musculus cDNA clone 78A01, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Joh, T., Yasunaga, T. and Shimada, K.
A catalogue of genes in mouse embryonal carcinoma F9 cells identified with expressed sequence tags
J. Blochem. 119, 749-767 (1996)
On Sep 12, 1996 this sequence version replaced gi:1405026.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 308)
Nishiguchi,S., Sakuma,R., Nomura,M., Zou,Z., Jearanaisilavong,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D76822.1 GI:1596557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Department of Medical Genetics, Division of Molecular Biomedicine Research Institute for Microbial Diseases, Osaka University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Kazunori Shimada
                                                                                                                                                               Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   house mouse
                                                                                                                                                                                                                                                                                82
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                                                                                                                   72.00
1.756
51.899
                                                                                                                                                                                                                                                                              /clone_lib="mouse embryonal carcinoma cell line F9" 74\ c 91 g 57\ t 4 others
                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:10090"
/clone="78A01"
                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
       from:
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                                                                                                                      Percent Identity: 30.380
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       to: 308
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DEFINITION
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              219 AGTTATCACCATCATGCAGAACCCACGACAGTACAAG 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37 CCTGAGAAGTTCCAGCACATTTTGCGAGTACTCAACACCAACATCGATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 ProAsnArgArgValPheIleLysArgValSerAsnValIleIleHisGl 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 yIleIleAlaAlaTyrGlnAsnProAlaSerTrpLys 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52 IleSerLeuLysLeuThrSerGlyLysIleAlaSerArgArgValAspGl 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45 hrIleGlyThrGlyArgArg.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28 yArgArgIleAspIlePheAlaSerLysAsnPheHisLeuGlnLysAsnT 45
                                                                                                                                                                                                                                                                                                                                                                  source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          np06all.sl NCI_CGAP_Pr3 Homo sapiens cDNA clone IMAGE:1115516 similar to gb:X69150 40S RIBOSOMAL PROTEIN S18 (HUMAN);, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA Library Preparation: David B. Krizman, Ph.D. CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1997)
on Sep 12, 1996 this sequence version replaced gi:1394196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 583)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; 
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA603354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA603354.1
                                                                                                                                                                                                                                                                                                                                                                                                                 Insert Length: 635 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 437.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D., Michael Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: (301) 496-1550
/note="Yector: pamp10; Site_1: Not1; Site_2: EcoRI; 1st strand cDNA was primed with oligo(dT)17 on 50 ng of pNAse-treated, total cellular RNA obtained from 5,000-10,000 microdissected cells histologically-determined to be fully malignant prostate cancer cells. Double-stranded cDNA was ligated to EcoRI.
                                                                                                                                                                                                                                                                                          /db_xref="taxon:9606"
/map="8"
                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
                                                                                                                                                        /dev_stage="45 years old"
/lab_host="DH10B"
                                                                                                                                                                                                                                     /clone_lib="NCI_CGAP_Pr3"
                                                                                                                                                                                                                                                              /clone="IMAGE:1115516"
                                                                                                                                                                                                                                                                                                                                                                                           Cocation/Qualifiers
                                                                                                                                                                                                                  /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GI:2437215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    583 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: gb_est13:AA372511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to reverse of: AA603354 from: 1 to: 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-142-524-1 x AA603354/rev ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                374 TGTGATCACCATTATGCAGAATCCACGCCAGTACAAG 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 424 ATTGACCTCACCAAGAGGGCGGGAGAACTCGCTGAGGATGAGGTGGAACG 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           469 .....GGTGTGGGCCGAAGATATGCTCATGTGGTGTTGAGGAAAGCAGAC 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               506 GCGGCGAAAATAGCCTTTGCCATCACTGCCATTAAG...... 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            556 CCTGAAAAGTTCCAGCATATTTTGCGAGTACTCAACACCAACATCGATGG 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 yIleIleAlaAlaTyrGlnAsnProAlaSerTrpLys 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52 IleSerLeuLysLeuThrSerGlyLysIleAlaSerArgArgValAspGl 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28 yArgArgIleAspIlePheAlaSerLysAsnPheHisLeuGlnLysAsnT 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 ProAsnArgArgValPheIleLysArgValSerAsnValIleIleHisGl 28
Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
Bult.C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
Kelley,J.G., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligtino,S.M.,
Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
Bednarik,D.P., Cao,L., Cepeda,M.A., Fischer,C., Hastings,G.A.,
He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
Billion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
Initial assessment of human gene diversity and expression patterns
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 343)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST84502 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to ribosomal protein S18, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ÃÃ372511.1 GI:2024904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    numan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74.00
1.805
51.899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   adaptors, 5 cycles of PCR applied to the cDNA with an adaptor specific primer, and the resulting PCR product subcloned into pAMPI0 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by David Krizman."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     343 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               161 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Identity: 31.646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA
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KEYWORDS
                                                                                                                                                                                                                       DEFINITION
                                                                                                                                                                                                                                                             seq_documentation_block:
                                                                                                                                                                                                                                                                                                          seq_name: gb_est14:AA381359
                                                                                                                                                                             ACCESSION
                                                                                                                                     ERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality: 72.00
Ratio: 1.714
Percent Similarity: 53.165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMMENT
                                                                 ORGANISM
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                                                                                                                                                                                                                                                                                                                                          214 TGTGATCACCATTATGCAGAATCCACGNCAGTACAAG 250
                                                                                                                                                                                                                                                                                                                                                                                                                               164 ATTGACCTCACCAAGAGGGCGGGAGAACTCACTGAGGATGAGGTGGAACG 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119 .....GGTGTGGGCCGAAGATATGCTCATGTGGTGTTGAGGAAAGCAGAC 163
                                                                                                                                                                                                                                                                                                                                                                                  68 yIleIleAlaAlaTyrGlnAsnProAlaSerTrpLys 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52 IleSerLeuLysLeuThrSerGlyLysIleAlaSerArgArgValAspGl 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45 hrileGlyThrGlyArgArg......51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28 yArgArgIleAspIlePheAlaSerLysAsnPheHisLeuGlnLysAsnT 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 ProAsnArgArgValPheIleLysArgValSerAsnValIleIleHisGl 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCTGAAAAGTTCCAGCATATTTTGCGAGTACTCAACACCAACATCGATGG 81
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                               EST94431 Activated T-cells I Homo sapiens CDNA 5' end similar to similar to ribosomal protein S18, mRNA sequence.
                                                                                                           EST
                                                                                    numan
                                                                                                                            ĀA381359.1 GI:2033679
                                                                                                                                                        g2033679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  On May 8, 1995 this sequence version replaced gi:800909.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Index (http://www.tigr.org/tdb/hgi/hgi.html)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: arkerlay@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9712 Medical Center Drive, Rockville, MD 20850 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Organ: colon; Vector: pBluescript SK-; Site_1:
ECORI; Site_2: XhoI"
75 c 90 g 74 t 5 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organish="Homo sapiens", /db_xref="ATCC (inhost):176944"
/db_xref="taxon:9606"
/clone_lib="Colon adenocarcinoma IV"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                   263 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Identity: 30.380
                                                                                                                                                                                                                                     mRNA
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: AA381359 from: 1 to: 263
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Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr.,
Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M.,
Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
Moreno, J.M., Gruber, J., Hudson, P., Kim, A.K.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,
Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
Praser, C.M. and Venter, J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
AL Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                45 hrlleGlyThrGlyArgArg..... 51
                                                                                                                                                                                                                                          28 yArgArgIleAspIlePheAlaSerLysAsnPheHisLeuGlnLysAsnT 45
                                                                                                                                                                                                                                                                                                                                                                    43 CCTGAAAAGTTCCAGCATATTTTNCGAGTACTCAACACCCAACATCGATGG 92
                                                                                                                                                                                                                                                                                                                                                                                                                                      12 ProAsnArgArgValPheIleLysArgValSerAsnValIleIleHisGl 28
52 IleSerLeuLysLeuThrSerGlyLysIleAlaSerArgArgValAspGl 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bioinformatics
The Institute for Genomic Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96026280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: arkerlav@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sep 12, 1996 this sequence version replaced gi:1405101
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1.732
51.899
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/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Activated T-cells I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="ATCC (inhost):185717"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Identity: 30.380
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                                                                                alignment_scores:
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                                                                                                                                                                                                         BASE COUNT
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 yIleIleAlaAlaTyrGlnAsnProAlaSerTrpLys 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
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Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
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Dinke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
Dinke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
Kaymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
Fristell secretain of human can diversity and avvracein natterns
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Seq primer: M13 Reverse.
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The Institute for Genomic Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9712 Medical Center Drive, Rockville,
                                                          Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: arkerlav@tigr.org
                                  Ratio:
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                                                                                                                                                                                                         /note="Organ: skin; Vector: pBluescript SK-; Site_1:
ECORI; Site_2: XhoI"
65 c 71 g 57 t 3 others
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   71.00
1.732
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                                                                                                                                                                                                                                                                                                                                                       /db_xref="ATCC (inhost):183986"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="ATCC (inhost):
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FEATURES
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                                                                                                                                                                                                                                source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       127 .....GGTGTGGGCCGAAGATATGCTCATGTGGTGTTGAGGAAAGCAGAC 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68 yIleIleAlaAlaTyrGlnAsnProAlaSerTrpLys 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45 hrIleGlyThrGlyArgArg.....51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40 CCTGAAAAGTTCCAGCATATTTINCGAGTACTCAACACCAACATCGATGG 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 ProAsnArgArgValPheIleLysArgValSerAsnValIleIleHisGl 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mouseest@watson.wustl.edu
This clone is available royalty free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                            Contact: Marra M/Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tal: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                Seq primer: -28m13 rev1 ET from Amersham High quality sequence stop: 168.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Marra,M., Hiller,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mr52c03.r1 Life Tech mouse embryo 15 5dpc 10667012 Mus musculus cDNA clone IMAGE:601060 5' similar to gb:M76763 Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ribosomal protein (MOUSE);, mRNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to: AA379609 from: 1 to: 268
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/db_xref="taxon:10000"
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/dev_stage="15.5dpc embryos"
/lab_host="DH10B"
                                                                                                                                                                          /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                            ocation/Qualifiers
                                                                                                                                                                                                                              .490
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VERSION
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US-09-142-524-1 x AA288347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             203 ACTCACGGAGGATGAGGTGAGCGAGTGATCACCATCATGCAGAACCCAC 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    253 GACAGTACAAG 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              153 CATGTGGTGTTGAGGAAAGCAGACATCGACCTCACCAAGAGGGGCTGGAGA 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 CTGCCATTAAG........GGCGTGGGGGCGGAGATATGCT 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 sileAlaSerArgArgValAspGlyIleIleAlaAlaTyrGlnAsnProA 77
Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pellgyrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kin, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C. M. and Venter, I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77 laSerTrpLys 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52 .....IleSerLeuLysLeuThrSerGlyLy 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37 ysAsnPheHisLeuGlnLysAsnThrIleGlyThrGlyArgArg..... 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71 AGTACTCAACACCAACATCGATGGGCGGCGGAAAATAGCCTTCGCCATCA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20 gValSerAsnValIleIleHisGlyArgArgIleAspIlePheAlaSerL 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 ACCGCCGCCATGTCTATGTGATCCCTGAGAAGTTCCAGCACATTTTGCG 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 ThrValAlaPheAsnGlnPheGlyProAsnArgArgValPheIleLysAr 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA378031 287 bp mRNA EST 21-APR-19
EST90680 Synovial sarcoma Homo sapiens cDNA 5' end similar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similar to ribosomal protein S18, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA378031.1 GI:2030349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 287)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ratio:
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52.874
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Identity: 29.885
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JOURNAL
MEDLINE
COMMENT
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ORIGIN
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US-09-142-524-1 x AA378031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality: 71.00
Ratio: 1.732
Percent Similarity: 51.899
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
                                                                                       170 ATTGACCTCACCAAGAGGGCGGGAGAACTCACTGAGGATGAGGTGGAACG 219
                                                                                                                                                                              125 .....GGTGTGGGCCGAAGATATGCTCATGTGGTGTTGAGGAAAGCAGAC 169
220 TGTGATCACCATTATGCAGAATCCACGCCAGTACAAG 256
                                                                                                                                                                                                                                                                                                                                                               38 CCTGAAAAGTTCCAGCATATTINGCGAGTACTCAACACCAACATCGATGG 87
                                                                                                                                                                                                                                                                                                                                                                                                         12 ProAsnArgArgValPheIleLysArgValSerAsnValIleIleHisGl 28
                                                                                                                                                                                                                          45 hrileGlyThrGlyArgArg..... 51
                                                                                                                                                                                                                                                                        28 yArgArgIleAspIlePheAlaSerLysAsnPheHisLeuGlnLysAsnT 45
                                                                                                                                   52 IleSerLeuLysLeuThrSerGlyLysIleAlaSerArgArgValAspG1 68
                          68 yIleIleAlaAlaTyrGlnAsnProAlaSerTrpLys 80 :::|||::: |||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M.3 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995) 96026280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Kerlavage, AR
Bioinformatics
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    On Sep 12, 1996 this sequence version replaced gi:1395403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
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/tissue_type="adult, 20 yrs"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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C
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Gaps: 2
Percent Identity: 30.380
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